Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

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83.2
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6/ptodata/2/pna/US6006_COMB.seq:
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have ε score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 1. Appli	Sequence 2. Appli	Sequence 2, Appli	1059.	Sequence 2370, Ap	equence 74	equence 74		equence 58	58	12	٠,	a		edneuce	ednence	Sequence 753, App	Sequence 10, Appl	Sequence 10, Appl	(1)	4	Sequence 4, Appli	41	Sequence 2371, Ap					equence 1	Sequence 15, Appl	Sequence 5056, Ap
		ID	US-09-763-292-1	-07-864-	US-08-238-821A-2	55-105	07 - 23	76-74	68-7	1-74	27-5	27B-5	10-1	79	US-09-023-655-1057	US-09-135-296-4	76-75	68-7	71-75	2C-10	238-821A-1	5-09-471-275-	-864-962C	-238-821A-	-09-023-655-1	-09-880-107-2	-60-172-373-	-60-226-176-7	0-233-468-7	-60-313-371-7	-08-277-031A-1	08-277-031B-1	-360-5
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		Score	1746	1739.6	1739.6	1739.6	1739.6	1739.6	1739.6	1739.6	1739.6	1739.6	1625.2	1534.6	1534.6	1534.6	1534.6	1534.6	1534.6	1534.5	1534.6	1534.6	1529.8	1529.8	1529.8	1529.8	1512.6	1456.6	1466.6	1466.6	1458.6	1458.5	1453.2
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Sequence 15325, A Sequence 14, Appl Sequence 14, Appl Sequence 2, Appl Sequence 754, App Sequence 754, App Sequence 754, Appl Sequence 2, Appli Sequence 2, Appli Sequence 1055, Appl Sequence 1055, Appli Sequence 6, Appli Sequence 6, Appli		Length 1746: Indels 0: Gaps 0 tgcttctcctttcaa 60
1836 65 US-60-324-185-25325 3 1892 3 US-07-864-962C-14 1892 6 US-08-238-821A-14 1591 5 US-08-194-981C-2 2 880 60 US-60-226-176-754 1 1473 55 US-60-226-176-754 1 1473 64 US-60-313-448-754 1 1473 6 US-60-313-371-754 1 1473 6 US-08-194-981C-3 1 1419 5 US-08-194-981C-3 1 1995 14 US-09-023-655-1055 1 2009 3 US-08-238-821A-6	ESULT S-09-763-292-1 S-09-763-292-1 S-09-763-292-1 S-09-763-292-1 S-09-763-292 GENERAL INFORMATION: APPLICANT: AB Sangtec Medical TITLE OF INVENTION: New method FILE REFERENCE: primers CURRENT APPLICATION NUMBER: US/09/763,292 CURRENT FILING DATE: 2000-02-21 SOFTWARE OF SEQ ID NOS: 19 SOFTWARE: PatentIn Ver: 2.1 LENGTH: 1746 LENGTH: 1746 LENGTH: 1746 S-09-763-292-1	itch 30.0%; Score 1746; DB 30; Length 174 100.0%; Pred. No. 0; Indels 0 ctcaatgatccttttgtggtccttgtctctctatgtttgcttctctcttcttcttcttcttcttgtggtccttgtgtctctctcttgtgtttgcttctctctcttttgtggtccttgtgtctctgtctctctcttct
1453.2 83.2 1436.4 82.3 1373.6 78.7 1371.6 78.6 1346.6 77.1 1346.6 77.1 1345.6 77.1 1343.4 76.9 1343.4 76.9 1264.6 72.4 1264.6 72.4	SULT 199-763-29-1 Sequence 1, Applica GENERAL INFORMATION APPLICANT: AB Sanc TITLE OF INVENTION FILE REFERENCE: DE CURRENT APPLICATION CURRENT FILING DAI NUMBER OF SEG ID N SOFTWARE: PATENTING LENGTH: 1746 TYPE: DNA ORGANISM: HOMO SB ORGANISM: HOMO SB	Ouery Match Best Local Similarity Matches 1746; Conserv. 1 cttcaatggatcct

ttccccagatctaggaacattcagctc 1620 ttctgctattccccatactctataggtac 1680 liiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii		0y 121 tratggaaagtgatattttggagaaagtaaaagtacaattactaaaaactggtgct / 20 0y 721 ttatggaaagtgatattttggagaaagtaaaagaacccaagaatcgatggacatcact
1561 tcttctgacccgtcatctccatttcccttcc 1621 cattaaaaaagtttcactgtgcaaatatctg 1631 attgagtgccacataatgctgaaatatctg 1681 attgagtgccacataatgctgaaatatctg 1681 attgagtgccacataatgctgatacttgtctaa 1681 attgagtgccacataatgctgatacttgtctaa 171 aataga 1746 1741 aataga 1747 1741 aataga 1746 1741 aataga 1747 1751 aataga 1747 1751 aataga 1742 1751 aataga 1746 1751 aataga 1746	cttccccaagatctagtgaacattcagcctc 1620 atctgctattccccatactctaatagttac 1680 illi	DOS/MS-DOS lease #1.0, Version #1.25 \$/07/864,962C ON: 26,581 R: WTS/5683/92024 ATION: 00 2: 5%: Score 1739.6; DB 3: Length 1746; 8%: Pred. No. 0; 0: Mismatches 4; Indels 0; Gaps 0; 99tccttgtgctctgtctctatgtttgcttctcttcaa 60 1

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0; Mismatches
                                                                                                                                                                                                                 99.6%; Score 1739.6; 99.8%; Pred. No. 0;
    REFERENCE/DOCKET NUMBER: 15280-192-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1746 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                         Best Local Similarity 99.8 Matches 1742; Conservative
                                                                                                                                                LOCATION: 1.5
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                     NAME/KEY: Region
LOCATION: 1..5
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                                                                                                                                                                                                                  Query Match
                                                                                                                           FEATURE:
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GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, JOYCE A.
APPLICANT: ROMES-TIN, JOYCE A.
APPLICANT: ROMES-SPARKS, Marjorie
TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
TITLE OF INVENTION: SUBFAMILY
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                               1201 AAGAATTTCCCAACCCAGAGATGTTTGACCCTCGTCACTTTCTGGATGAAGGTGGAAATT 1260
                    Cre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend and Townsend Khourie
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PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 379 Lytton Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: 116
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                                                            1621 CATTAAAAAAGIIICACTGTGCAAATATATCTGCTATTCCCCATACTGTATAATAGTAAC
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RESULT 4 US-09-023-655-1059

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                                                                      THE
                      APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE
TITLE OF INVENTION: EXPRESSION
NUMBER-OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, IN
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/023,655 FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PA-0001 TELECOMMUNICATION INFORMATION:
Sequence 1059, Application US/09023655 GENERAL INFORMATION:
                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEO 1D NO: 1059:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  37,071
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 1746 base pairs
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-09-023-655-1059
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                                                                                                                                                                                                94304
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Workley, Joseph G.
APPLICANT: Workley, Joseph G.
APPLICANT: Workley, Joseph G.
APPLICANT: Gene Lot, Uwe
APPLICANT: Gene Expression Profiles in Liver Cancer: ITILE OF INVENTION: Gene Expression Profiles in Liver Cancer: FILE REFERENCE: 44921-5028-w0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/231,379
PRIOR FILING DATE: 2000-10-02
NUMBER OF SED ID NOS: 3950
SOFTWARE: PARCETIN VOIL 12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Genbank Accession No. M61854
9-880-107-2370
                                                                                                                                                                                                                                                                                                                                                                     quence 2370, Application US/09880107 NERAL INFORMATION:
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ORGANISM: Homo sapiens
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9-880-107-2370
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LENGIH: 1746
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y 241 gatatgaagtggtgaaggaagccctgattgatctttgatctttggaagagtttttctggaagaggcc 300 i	301 atttcccactggctgaaagagctaacagaggatttgaatcgtttcagcaatggaaaga 36	361 gatggaaggagattcggcgtttctc 	421 ggagcatt 421 ggagcatt	481 ccaaggttcaccctgtgatcccacttcatcctggg 	541 gctccattattttccagaacgttt 	/ 601 aaaaattgaatgaaacatcaggattgtaagcacccctggatccagatatgcaataatt 660 	 661 ttcccactatcattgattattcccgggaacccataacaaattacttaaaaaccttgctt 720 111111111111111111111111111111111111	/ 72] ttatggaaagtgatatttggagaaagtaaaagaacaccaagaatcgatggacatcaaca 780 	781 accctgggactttattgattgcttcctgatcaaaatggagaaggaaaagcaaaacgaac 840 	 841 agtctgaattcactattgaaaacttggtaatcactgcctgacttactt	 901 cagagacaacaagcacaaccctgagatatgctctccttcct	 961 tcacagctaaagtccaggaagaqttgaacgtgtcattggcagaaaccggagccctgca 1020 111111111111111111111111111111111111	1021	1081 tcgacctcatcccaccagcctgccccatgcagtgacctgtgacgttaaattcagaact 1140 	1141 accteattcccaagggcacaaccatattaacttccctcacttctgtgctacatgscaaca 1200	 1201 aagaatttcccaacccagagatgtttgaccctcgtcacttctggatgaaggtggaaatt 1250 111111111111111111111111111111111111	1261 ttaagaaaagtaactacttcatgcctttctcagcaggaaaacggatttgtgtgggaagagg 1320 	1321 goctggcccgcatggagctgttttattcctgaccttcattttacagaactttaacctga 1380
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Malsen, Gareth
Townley, David
Morris, MacDonald
VENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
NCE: GX-0013-1 P
LICATION NUMBER: US/60/226,176
LING DAIE: 2000-08-16
SED ID NOS: 2447
PERL Program
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.larity 99.8%; Pred. No. 0;
Conservative 0; Mismatches
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WATION: GB:HUMCYPC219
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Db 1261 ttaagaaagtaactacttcatgccttctcagcaggaaaacggatttgtgtgggagagg 1320 Oy 1321 gcctggcccgcatggagctgtttttattcctgaccttcattttacagaactttaacctga 1380	Oy 1381 aatctctgattgacccaaaggaccttgacacaactcctgttgtcaatggatttgcttctg 1440 	Oy 1441 tecegecettetateagetgtgetteatteetgtetgaagaageacagatggtetggetg 1500 	Oy 1501 ctcctqtgcqtctctttcctctggtccaaatttcactatctgtgatgct 1560	Oy 1561 tettergaccegteateteacatttteeetteececaagatetagtgaacatteageete 1620 	Oy 1621 cattaaaaaagtttcactgtgcaaatatatctgctattccccatactctataatagttac 1680 	Oy 1681 attgagtgccacataatgctgatacttgtctaatgttgagttattaacatattatta 1740 	Oy 1741 aataga 1746 	RESULT 7 7 4 9 US-60-233-468-749 Sequence 749, Application US/60233468	: GENERAL INFORMATION: ; APPLICANT: Ring, Huijun 2. ; APPLICANT: Malsen, Gareth ; APPLICANT: Davidy.	: APPLICANT: Morris, MacDonald : APPLICANT: Valdes, Ana : ITILE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes : FILE REFERENCE: GX-0013-2 P	CURRENT APPLICATION NUMBER: US/60/233,468 CURRENT FILING DATE: 2000-09-18 NUMBER OF SEQ ID NOS: 2488 SOFTWARE: PERL Program	SEQ 1D NO 749 SLENGTH: 1746 TYPE: DNA CRGANISM: Homo sapiens	FEATURE: NAME/KEY: misc_ OTHER INFORMATI 5-60-233-468-749	Score 1739.6; DB 56; Length 1746; Pred. No. 0;	1/42; Conservative 1/42; Conserv	Oy 61 tctgaatggatccttttgtggtccttgtgctctgtctctcatgtttgcttctcttcaa 60 Oy 61 tctggaacagagctctgggaagagaaaactcctcctgggcccactcctcccagtga 120 Db 61 tctggaacagaactctgggaagagaaaactccttctctcactgtcactagta 120 Db 61 tctgaacagaactctagaaaaaactcctagaaaaactcacaactaataataataa	ttggaaatateetacagatagatattaaggatgteagcaaateettaaceaateteetea 18
Db 181 aaatctatggcctgtgttcactctgtattttggcctggaacgcatggtgtgctgcatg 240 Oy • 241 gatatgaagtggtgaaggaagcctgattgatcttggagaggagtttctggaagaggcc 300 Db 241 gatatgaagtggtgaaggaagccctgatttgatcttggagaggagtttctggaagaggcc 300 Db 241 gatatgaagtggtgaaggaagccctgattgatcttggagaggaqtttcttggaagaggcc 300	tggctgaaagagctaacagaggatttggaatcgttttcagcaatggaaaga 	attttgggatggggaaga 4 	aggagttgagaaaaa 4 	rgtgctccctgcaatgtg 	Oy 541 getecattatttecegaaaegtttegattataaagateaegaatteetaaettgatgg 600 	Oy 601 aaaaattgaatgaaaacatcaggattgtaagcacccctggatccagatatgcaataatt 560 	9ggaacccataacaaattacttaaaaaccttgctt 7 	Oy 721 ttatggaaagtgatattttggagaaagtaaaagaacaccaagaatcgatggacatcaaca 780 	 781 accetoggaetttattgattgetteetgateaaatggagaaggaaagcaaaceaee 840 111111111111111111111111111111111111	Oy 841 agtotgaattoactattgaaaacttggtaatoactgoagctgacttacttggagctggg 900 	Oy 901 cagagacaacaagcacaacctgagatatgctctcttctctgtgaagcacccagagg 960 	Oy 961 tcacagctaaagtccaggaagagttgaacgtgtcattggcagaaaccggagcccctgca 1020 	Oy 1021 tgcacgacagggccacatgccctacacagatgctgtgqtgcacgagqtccagagataca 1080 	1081 togacctcatcccaccagcctgcccatgo	2y 1141 acctrattcccaagggcacaaccatattaacttccctcacttctgtgctacatgacaaca 1200 	1201 aagaatttcccaacccagagatgtttgacctcgtcactttctggatgaaggtggaaatt [11] [11] [11] [11] [11] [11] [11] [1	vy izoi utaagaaaguaactacttcatgcctttctcagcaagaaaacggatttgtgtgtg

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NI: Ring, Huljun 2.
NI: Ring, Huljun 2.
NI: Massen, Gareth
NI: Townley, David
NI: Morris, MacDonald
NI: Morris 0; agaatttoccaacccagagatgtttgaccctcgtcactttctggatgaaggtggaaatt 1260 rijagagacagagetetgggagagaaaaeteeeteggeeeeaeteeteteeeagtga 120 Gaps DB 64; Length 1746; ; 0 4; Indels 99.6%; Score 1739.6; 99.8%; Pred. No. 0; 0; Mismatches 71-749 749, Application US/60313371 NFORMATION: Y: misc_feature NFORMATION: GB:HUMCYPC219 71-749 l Similarity 99.8 742; Conservative 1: Homo sapiens ataga 1746 |||||| |staga 1746

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Sequence 58, Application US/09488127 GENERAL INFORMATION:
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Best Local Similarity
Matches 1742; Conserv
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; ORGANISM: HOMO
US-09-488-127-58
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1740 Gaps 60 Length 1748 .; 4; Indels STRUCTURE 18; DB GENE Score 1739.6; pred. No. 0; 0; Mismatches APPLICANT: Thomann, Hans-Ulrich
APPLICANT: Thomann, Hans-Ulrich
TITLE OF INVENTION: RAPID DETERMINATION OF
TITLE OF INVENTION: USING CDNA SEQUENCE
FILE REFERENCE: 2709.1005-000
CURRENT APPLICATION NUMBER: US/09/488.127
CURRENT FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0 OF

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GENERAL INFORMATION:
APPLICANT: Williamson, Mark
ITILE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
ITILE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2099-001
CURRENT APPLICATION NUMBER: US/09/698,010
CURRENT FILING DATE: 2000-10-27
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 15684
SOFTWARE: FastSEQ for Windows Version 4.0
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96.3%; Pred. No. 0;
tive 0; Mismatches
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LCCATION: (1)...(1940)
: OTHER INFORMATION: n = A,T,C or G
US-09-698-010-12366
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Best Local Similarity 96.38
Matches 1691; Conservative
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ORGANISM: Homo sapiens
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Oy Dp	248	agtggtgaaggaagcoctgattgatottggagaggttttotggaagaggcoatttoco 307
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Qy Dp	548	tattttccagaaacgittcgattataaagatcacgaatttcttaacttgatggaaaaatt 507
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Oy Db	668	tatcattgattatttcccgggaacccataacaaattacttaaaaaccttgcttttatgga 727
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Qy Db	788	ggactttattgattgcttcctgatcaaaatggagaaggaaaagcaaaaccaacagtctga 847
Qy Db	848	attcactattgaaaacttggtaatcactgcagctgacttactt
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Qy Db	1088	catcccaccagcctgcccatgcagtgacctgtgacgttaaattcagaaactacctcat 1147

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TITLE OF INVENTION: FUNCTIONAL BACTERIAL/MAMMALIAN CYTOCHROME P450 CHIMERA
FILE REFERENCE: 176/60232
CURRENT APPLICATION NUMBER: PCT/US98/16979
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 60/056,754
EARLIER FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 4
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Pred. No. 0;
0; Mismatches 109; Indels
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APPLICANT: University of Rochester: TILE OF INVENTION: FUNCTIONAL BACTERIA; CURRENT APPLICATION NUMBER: PCT/US98/16; CURRENT FILING DATE: 1998-08-17; EARLIER APPLICATION NUMBER: 60/056,754; EARLIER FILING DATE: 1997-08-20
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Best Local Similarity 92.9%:
Matches 1637; Conservative C
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ORGANISM: mammalian
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RESULT 13
US-09-023-655-1057
i Sequence 1057, Application US/09023655
: GENERAL INFORMATION:
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 314 PORTER DRIVE
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPASIBLE
COMPUTER: IBM PC COMPASIBLE
COMPUTER: BADDRES: US/09/023,655
FILING DATE: HERWAITH
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE:
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                                                                                                                            Score 1534.6;
Pred. No. 0;
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1057:
SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
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                                                                                                                                       Conservative
                                                                    TYPE: nucleic acid STRANDEDNESS: single
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CLONE: 9181302
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IMMEDIATE SOURCE:
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GENERAL INFORMATION:
APPLICANT: Jones, Jeffrey P.
APPLICANT: Shimoji, Miyuki
ITILE OF INVENTION: FUNCTIONAL BACTERIAL/MAMMALIAN CYTOCHROME P450
CURRENT APPLICATION NUMBER: US/09/135,296
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 60/056,754
EARLIER FILING DATE: 1997-08-20
NUMBER OF ENG ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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Pred. No. 0;
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ilarity 92.9%;
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CORGANISM: mammalian
US-09-135-296-4
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Matches 1637;
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Pred. No. 0;
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              APPLICANT: Malsen, Gareth
APPLICANT: Malsen, Gareth
APPLICANT: Townley, David
TILLE OF INVENTION: Single Nucleotide Polymerine Perpendicant Carolla-19, CURRENT APPLICATION NUMBER: US/60/226,176; CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2447
SEQ ID NO 753
    Sequence 753, Application US/60226176 GENERAL INFORMATION:
                                                                                                             ; NAME/KEY: misc_feature
; OTHER INFORMATION: GB:HUMCYP2C9A
US-60-226-176-753
                                                                                                                                              87.9%;
92.9%;
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                                                                                            TYPE: DNA
ORGANISM: HOMO
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: GENERAL INFORMATION:
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US-10-105-299-7201
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Sequence 1204, A
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Sequence 12117, A
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Sequence 21327, A
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(gan2_6/ptodata/2/pna/USO5_NEW_COMB.seq:*):

(gan2_6/ptodata/2/pna/USO7_NEW_COMB.seq:*):

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                             Compugen Ltd
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429, APP
12136, A
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TILE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT PPLIATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed · See File Wrapper or Palm
SOFTRARE: Patentin Ver. 2.0
SEQ ID NO 7201
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US-09-978-681A-429
US-09-978-56A-429
US-09-999-831A-429
US-09-999-829A-429
US-10-013-921A-429
US-10-013-921A-429
US-10-013-921A-429
US-10-013-929A-429
US-10-105-299-12136
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US-10-105-299-6774
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IIIE CF INVENTION: Human Secreted Proteins
IIIE CF INVENTION: Human Secreted Proteins
FILE REFERENCE: 90550
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEO ID NOS: 15197
Prior Application removed - See File Wrapper or 15 SCFIWARE: Patentin Ver. 2.0
SEC ID NO 12104
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Pred. No. 0.03
0: Mismatches
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NUMBER OF SEQ ID NOS: 31255
SEQ ID NO 20507
LENGIH: 256
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APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck or Phomes J.
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molec: 98 Associated With
ITILE OF INVENTION: Plants
TILE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT APPLICATION NUMBER: US/09/263,191
PRIOR FILING DATE: 1999-03-05
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                                                                                                          Ouery Match
4.7%: Score 35; DB 5; Length 111:5;
Best Local Similarity 55.3%; Pred. No. 1.2;
Matches 68: Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
IIILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PU207C1
CURRENT APPLICATION NUMBER: US/10/103.313
CURRENT FILING DAIE: 2002-03-12
NUMBER OF SEO ID NOS: 653
SOFIVER: Prior Application removed - See File Wrapper or Palm
SOFIWARE: PATENTIN Ver. 2.0
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                 : TYPE: DNA
: ORGANISM: Homo sapiens
US-10-105-299-12104
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Best Local Similarity
Matches 75; Conserv
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LENGIH: 11146
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                                                                                                                                                 Length 266;
                                                                                                                                                                                       90; Indels
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IIILE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DAIE: 2002-03-26
NUMBER QE_SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm Science Patentin Ver. 2.0
SEC ID NO 12317
LENGTH: $2845
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4.5%: Score 33.8; DB 5;
Best Local Similarity 51.6%; Pred. No. 0.41;
Matches 97; Conservative 0; Mismatches 90;
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Pred. No. 9.1;
0; Mismatches 98;
TYPE: DNA
OPGANISM: Glycine max
OTHER INFORMATION: Clone ID: 700958447H1
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Sequence 12317, Application US/10105299
SENERAL INFORMATION:
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"S-10-105-299-11849/c
' Sequence 11849, Application US/10105299
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Best Local Similarity 48.4%;
Matches 92; Conservative (
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: ORGANISM: Homo sapiens
!!S-10-105-299.12317
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us-09-763-292-2.rnpn

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APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Vicinity of Molecules and Other Molecules Associated With ITILE CF INVENTION: Plants
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4.3%: Score 32.2; DB 5; Length 261;
Best Local Similarity 57.4%; Pred. No. 1.2;
Matches 58; Conservative 0; Mismatches 43; Indels
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GENERAL INFORMATION:
APPLICANT: Barnes, Glenn T.
APFLICANT: Bertin, John
IIILE OF INVENTION: POLYMORPHISMS IN THE HUMAN CARD4 GENE
FILE REFERENCE: 07334-366601
CURRENT APPLICATION NUMBER: US/50/368,184
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ 1D MOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT FILING DATE: 2001-10-12
PRICE APLICATION NUMBER: US/09/263,191
PRICE FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 31255
SEQ ID NO 24327
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57.0%; Pred. No. 27;
live 0; Mismatches
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: ORGANISM: Glycine max
: OTHER INFORMATION: Clone ID: 700963405H1
US-09-975-254-24327
                                                                                                                                          Sequence 24327, Application US/09975254 GENERAL INFORMATION:
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: ORGANISM: Homo sapiens
US-50-258-184-1
                                                                                           RESULT 8
US-09-975-254-24327
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US-60-358-184-1/C
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APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Garier, Alexander
APPLICANT: Gordon, Brian
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TILE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF KIDNEY CANCER
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FRASEO for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.4%; Score 33; DB 5: Length 34762; Best Local Similarit; 53.5%; Pred. No. 8.5; Matches 59; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 4.4%; Score 32.8; DB 5: Length 272: Best Local Similarity 53.0%; Pred. No. 0.82; Matches 70: Conservative 0: Mismatches 52: Indels (
                 : NAME/KEY: misc_feature
... LOCATION: (19530)..(19530)
: OTHER INFORMATION: n equals a,t,g, or
US-10-105-299-11849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Sequence 480, Application US/10102524 : GENERAL INFORMATION:
                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-102-524-480
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2484 GGGAGGCCG 2476
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GENERAL INFORMATION:
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LENGIH: 272
                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                           FEATURE:
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73 cttagcaaatggacaaaatagtaacttcgtttgctgttatctctgtctactttcctagct 132
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APPLICANT: Rosen et al.

IIILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIG9701

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT APPLICATION NUMBER: US/22

PRIOR PAPLICATION NUMBER: 09/925,298

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-0

FRIOR FILING DATE: 1990-03-08

FRIOR FILING DATE: 1990-03-12

NUMBER OF SED ID NOS: 846

SCOTIWARE: PATCHILIN VET: 2.0

SCOTIWARE: PATCHILIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Overy Match 4.2%: Score 31: DB 6: Length 6833; Pest Local Similarity 46.2%; Pred. No. 15: Matches 103: Conservative 0: Mismatches 120: Indels
                                                             Sequence 7027, Application US/10105299
SEMPEAL INFORMATION:
FILE REFERENCE: PS950
CURRENT APPLICATION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105, 299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ 1D NOS: 15197
PTION APPLICATION TEMOVED - See File Wrapper or Palm
SEQ 1D NO 7023
LEMSTH: 6833
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: GENERAL INFORMATION:
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NAME/KEY: misc_feature
LCCATION: (20)
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OTHER INFORMATION: n equals
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US-10-105-299-7023
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ORGANISM: Homo sapiens
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LOCATION: (19)
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LOCATION: (295)
                                       US-10-105-299-7023
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TILE OF INVENTION: Colon and Colon Cancer Associated Polynuclectiises and Polypertide
CURRENT APPLICATION NUMBER: US/10/106,598
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US/10/106,598
PRIOR APPLICATION NUMBER: US/10/109-28
PRIOR PILING DATE: 1000-09-28
PRIOR PILING DATE: 1999-10-29
PRIOR PLING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
PRIOR PILING DATE: 1999-11-03
PRIOR PILING DATE: 1999-11-03
SOFTWARE: Patentin Ver. 3.0
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4.3%; Score 31.6; DB 6; Length 555;
Best Local Similarity 58.5%; Pred. No. 2.7;
Matches 55; Conservative 0; Mismatches 39; Indels
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TILE OF INVENTION: Human Polynucleotides and Polypeptides
TILE REPERNCE: 22846/1720
CURRENT APPLICATION NUMBER: US/09/789,189
PRIOR APPLICATION NUMBER: 60/183452
PRIOR FILING DATE: 2000-02-18
NUMBER OF SE0 ID NOS: 2005
SOFTWARE: PatentIn version 3.1
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59.8%; Pred. No. 2.8;
ttive 0; Mismatches 35; Indels
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US-10-106-598-785
: Sequence 786, Application US/10106598
: GENERAL INFORMATION:
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; Sequence 1604, Application US/09789189
; GENERAL INFORMATION:
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1071 AGTCAGGGGTGAGCA 1057
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Matches 52; Conservative
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; ORGANISM: Homo sapiens
US-10-106-698-786
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LENGIH: 256
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Pred. No. 5.5;
0; Mismatches 72; Indels
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CUPRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm SEQ ID NO 12428
LENGTH: 49375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
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US-10-105-299-12428/C
US-10-105-299-12428/C
SEQUENCE 12428. APPLICATE ROSEN, et. al
TILLE OF INVENTION: Human Secreted Proteins: FILE REFERENCE: PS950
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        : NAME/KEY: misc_feature
: LCCATION: (734)...(734)
: OIHER INFORMATION: n equals a,t,g,
US-10-106-698-1347
                                                                                                            Ouery Match
Best Local Similarity 50.7%;
Matches 74: Conservative
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Best Local Similarity 52.8%;
Matches 66; Conservative (
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; ORGANISM: HOMO :
US-10-105-299-12428
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SUBJECT INFORMATION:
SUBJECT INVENTION:
COLON and Colon Cancer Associated Polynumismides and Polyneptide
FILE PETERENCE: PA008791
CURRENT APPLICATION NUMBER: US/10/106, 699
PRIOR PAPLICATION NUMBER: US/10/2062624
PRIOR PAPLICATION NUMBER: US/10/2069-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PATCHTION VOWER: US 60/163, 280
PRIOR FILING DATE: 1999-11-03
SEQ ID NOS: 8564
SOFTWARE: PATCHTION VOWER: US 60/163, 280
PRIOR FILING DATE: 1999-11-03
SEQ ID NOS: 8564
SOFTWARE: PATCHTION VOWER: US 60/163, 280
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4.1%; Score 30.8; DB 5;
Best Local Similarity 51.2%; Pred. No. 5.2;
Matches 65; Conservative 0; Mismatches 62;
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LOCATION: (675)..(676) '
OTHER INFORMATION: n equals a,t,g, or
     INFORMATION: n equals a, t, q, or
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OTHER INFORMATION: n equals a, L, g, NAME/KEY: misc_feature
LAGATION: (512)
OTHER INFORMATION: n equals a, L, g, NAME/KEY: misc_feature
                                                                                   LOCATION: (552)
OTHER INFORMATION: n equals a.t.g.
NAME/KEY: misc_feature
LOCATION: (558)
                                                                                                                                                                                                     OTHER INFORMATION: n equals a,t,q,
                                                                                                                                                 OTHER INFORMATION: n equals a,t,g,
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LOCATION: (588)
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ORGANISM: Homo sapiens
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US-10-102-806-359
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April 19, 2002, 11:02:26 ; Search time 5830.82 Seconds (without alignments) 2760.419 Million cell updates/sec
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/cgn2_6/ptodata/2/pna/US6001_COMB.seq.
/cgn2_6/ptodata/2/pna/US6002_COMB.seq:
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/cgn2_6/ptodata/2/pna/US6005_COMB.seq:
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/cgn2_6/ptcdata/2/pna/US6008_COMB.seq:
/cgn2_6/ptcdata/2/pna/US6009_COMB.seq:
/cgn2_6/ptcdata/2/pna/US6010_COMB.seq:
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
. No.	Score	Match	Length DB	DB	QI	Description
1	7		743	30	US-09-763-292-2	Sequence 2 and
7	φ.		743	52	-60-226-176-75	75.0
m	•	•	743	99	-60-233-468-7	756
♥	ά.	•	74	64	-60-313-371-75	7.5
S	÷.		9	54	-60-212-657-15	
	'n.	98.1	76	54	-60-213-18	, 6
	\circ		95	57	-60-248-498-2	equence 20,
	\circ	٠	22	57	0-248-498-6	1 (
ر 0	708	95.3	222537	57	-60-248-542	3 6
-	70	95.3	25	57	-60-245-227-9	0
1		•	8437	18	-09-488	0
12		•	8437	18	-09-488-127B-5	0
13		٠	8437	18	-488-127B-	20
14		•	572	51		147
15			572	51	-60-182-895-1	148
16			572	51	-60-182-895-14	149
17			572	21	-89	150.
138			572	51	50-182-895-15	151
6 7			572	51	-60-182-895	152.
20			572	25	-60-198-818-1	18,
21	544.2	73.2	1580	54	-60-213-795-3	m
7 (1580	24	-60-213-795-4	46
7		71.7	722	25	-60-195-048-1	108,
c 24	532.4	71.7	722	25	-60-195-	109,
7 (521.2	70.1	710	53	-60-205-16	3, Ar
97	488 2	65.7	664	25	US-60-198-818-178	178
27	433.6	58.4	1001	56	US-09-671-317-49	6.6
c 28	433.6	٠. 80	32141	55	-60-239-	'n
59	433.6	58.4	36191	57	-498-	equence 23.
30	433.6	58.4	36584	23	-60-245-227-	10,
31	r	58.4	118047	23	US-60-248-498-59	59,

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APPLICANT:

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Pred. No. 3.3e-209,
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                               : Sequence 756, Application US/60226176
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            743
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: OTHER INFORMATION: GB:HUM2C9X02
US-60-226-176-756
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Best Local Similarity 99.7
Matches 741; Conservative
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ORGANISM: Homo sapiens
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100.0%; Score 743; DB 30;
Best Local Similarity 100.0%; Pred. No. 3.7e-210;
Matches 743; Conservative 0; Mismatches 0;
US-60-248-542-60

US-09-671-317-50

US-09-671-317-55

US-09-488-127-64

US-09-488-127-64

US-00-205-169-6

US-09-488-127-62

US-09-488-127-62

US-09-488-127-62

US-00-128-67-14

US-60-217-67-14

US-60-217-67-14

US-60-200-392-43

US-60-200-392-43
                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: AB Sangtec Medical
TITLE OF INVENTION: New method
FILE REFERENCE: primers
CURRENT APPLICATION INVERS: US/09/763,292
CURRENT FILING DATE: 2000-02-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09763292 GENERAL INFORMATION:
   436
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US-09-763-292-2
 RESULT 1
US-09-763-292-2
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ORGANISM: Homo sapiens
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APPLICANT: Malsen, Gareth
APPLICANT: Townley, David
APPLICANT: Morbis, MacDonald
APPLICANT: Mortis, MacDonald
APPLICANT: Waldes, And
TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
FILE REFERENCE: GX-0013-2 P
CURRENT APPLICATION NUMBER: US/60/233,468
CURRENT FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 2488
SSC ID NO 756
LENGTH: 743
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                                                                                                                                                                                                                                                                                                                                                           99.6%; Score 739.8; DB 56; 99.7%; Pred. No. 3.3e-209; iive 0; Mismatches 2;
                                                                                                                                                                                                       Sequence 756, Application US/60233468 GENERAL INFORMATION:
APPLICANT:
Ring, Huijun Z.
                                                                                                                                                          ; NAME/KET: misc_feature
; OTHER INFORMATION: GB:HUM2C9X02
US-60-233-468-756
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  Similarity
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US-60-233-468-756
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APPLICANT: Raisen, Gareth
APPLICANT: Malsen, Gareth
APPLICANT: Townley, David
APPLICANT: Townley, David
TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME CFILE REFERENCE: GX-0013-5 P
FULE REFERENCE: GX-0013-5 P
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 2447
SOFTWARE: PERL Program
SEQ ID NO 756
LENGTH: 743
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                                                                                                                                                                                                                                                                                                                                                                                                         : Sequence 756, Application US/60313371
: GENERAL INFORMATION:
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; OTHER INFORMATION: GB:HUM2C9X02
US-60-313-371-756
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Sequence 15, Application US/60212657
APPLICANT:
APPLICANT:
Beasley, Ellen
TITLE OF INVENTION:
TITLE OF INVENTION:
PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
FILE REPERENCE:
CLORGENT APPLICATION NUMBER:
US/60/212,657
CURRENT FILIG DATE:
NUMBER OF SEQ ID NOS: 303
SOFTAMER: FastSEQ for Windows Version 4.0

LENGTH: 7609
9
                 98.1%; Score 728.8; DB 54; Length
llarity 99.6%; Pred. No. 2e-205;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: HUMAN
US-60-212-657-15
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Best Local Simil
Matches 741; C
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APPLICANT: BEASLEY, Ellen
TILE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/213,181
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEO ID NOS: 261
SEO ID NO 56
SEO ID NO 56
LENGTH: 32768
RESULT 6
US-60-213-181-56
Sequence 56, Application US/60213181
GENERAL INFORMATION:
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: LOCATION: (1)...(32768)

: OTHER INFORMATION: n = ...

US-60-213-181-56
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ORGANISM: Human
FEATURE:
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TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/248,498
CURRENT FILING DATE: 2000-11-15
SOFTWARE: FastSEO for Windows Version 4.0
SEO ID NO 24
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                    Indels
   54;
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   .8; DB 5
4e-205;
 Score 728.8;
Pred. No. 4e-2
0; Mismatches
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APPLICANT: Beasley, Ellen
ITILE OF INVENTION: ISOLATED HUMAN
ITILE OF INVENTION: PROTEINS, NUCLE
ITILE OF INVENTION: DRUG-METABOLIZI
/ Match 98.1%;
Local Similarity 99.6%;
Nes 741; Conservative
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INGTH: 51955
Query Match
                 Matches
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                                                                           Length 51955;
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ISOLATED HUMAN PHASE I DRUG-METABOLIZING
PROTEINS, NUCLEIC ACID MOLECULES ENCODING
                                                                                           Indels
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                                                                         Score 708;
Pred. No. 8
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APPLICANT: Beasley, Ellen
IIILE OF INVENTION: ISOLATED HUMAN
IIILE OF INVENTION: PROTEINS, NUCLE
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                                         A, I, C
                                                                        95.3%;
ilarity 97.8%;
Conservative
TYPE: DNA

CRGANISM: HUMAN

FEATURE:

NAME/KEY: misc_feature

CATION: (1)...(51955)

COTHER INFORMATION: n = A,
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Best Local Similarity
Matches 728; Conserv
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    USES
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                                                                                                                                     Length 222537;
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND FILL REPEREED: CLOOO910
CURRENT APPLICATION NUMBER: US/60/248,498
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 264
SOFTWARE: EASLSEQ for Windows Version 4.0
SEQ ID NO 61
LENGTH: 22537
TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                   15; Indels
                                                                                                                                   Score 708; DB 57;
Pred. No. 1.6e-198;
0; Mismatches 15;
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                                                                                    : NAME/KET: misc_feature
: LOCATION: (1)...(222537)
: OTHER INFORMATION: n = A,T,C
US-60-248-498-61
                                                                                                                                  Query Match 95.3%;
Best Local Similarity 97.8%;
Matches 728; Conservative
                                                                              FEATURE:
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Sequence 62, Application US/60248542
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION:
FILLE OF INVENTION:
FILLE OF INVENTION:
FILLE REFERENCE:
CURRENT APPLICATION NUMBER: US/60/248,542
CURRENT FILLO DATE:
CURRENT FILLO DATE:
CURRENT FILLO DATE:
NUMBER: FSALED FOR WINDOWS: 342
SOFTWARE: FSALED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                             Length 222537;
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Pred. No. 1.6e-198;
0; Mismatches 15;
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Best Local Similarity 97.8%;
Matches 728; Conservative C
                                                                                                              : NAME/KEY: misc_feature
: LOCATION.a.edf)...(225337)
: OTHER INFORMATION: n = A,T,C
US-60-248-542-62
                                                                                                 ORGANISM: Human
                                                                                   222537
                                                                                           TYPE: DNA
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93.3%;
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LCCATION: (1)...(8437)
OTHER INFORMATION: n = A,T,C
US-09-488-127-59
                                                                                                                                                                                                                                                                                                                                                          Query Match 83.8°
Best Local Similarity 93.3°
Matches 694; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                               RESULT 11
US-09-488-127-59
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TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
FILE REFERENCE: CLOO0876
CURRENT APPLICATION NUMBER: US/60/245,227
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
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                                                                                                                                                                                                                                                                                        Query Match

95.3%; Score 708; DB 57; Length 2

Best Local Similarity 97.8%; Pred. No. 1.6e-198;

Matches 728; Conservative 0; Mismatches 15; Indels
                                 or G
                                                                                        Sequence 9, Application US/60245227

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN

TITLE OF INVENTION: PROTEING WITH
                                                                                                                                                                                                                                        NAME/KET: misc_feature

: LOCATION: (1)...(22532)

: OTHER INFORMATION: n = A,T,C

US-60-245-227-9
                                                                                                                                                                                                               TYPE: DNA ORGANISM: HUMAN
                                                                                                                                                                                                      LENGTH: 225532
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                Score 622.6; DB 18;
Pred. No. 9.7e-174;
0; Mismatches 45;
                                                                                                                                                                                Sequence 59, Application US/09488127
GENERAL INFORMATION:
APPLICANT: Thomann, Hans-Ulrich
APPLICANT: Thomann, Hans-Ulrich
TITLE OF INVENTION: RAPID DETERMINATION OF
TITLE OF INVENTION: USING CDNA SEQUENCE
FLLE REFERENCE: 2709,1005-000
CURRENT APPLICATION NUMBER: US/09/488,127
CURRENT FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 59
                                                                                                                                                                                                                          OF
                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 4.0
                                                                                                                             92647 GITGITAGCICATGIGAAGCAGGG 92624
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: LOCATION: : OTHER INF	LOCATION: LOCATION: OTHER INF	LOCATION: LOCATION: OTHER INFO	: LOCATION: : LOCATION: : OTHER INFO	LOCATION: LOCATION: OTHER INFO	LOCATION: LOCATION: OTHER INFC	LOCATION: LOCATION: COTHER INFO NAME/KEY: LOCATION:	LOCATION: OTHER INFC NAME/KEY: LOCATION:	OTHER INFO	OTHER INFO NAME/KEY: LOCATION: LOCATION:	OTHER INFO	CCATION: CCATION: COCATION: COCATION	Query Match Best Local S	Matches 694	Db 1391 tcag	07 61 tgct	0y 121 actt	1510	05 1569 catgo	Db 1629 gttt
Oy 421 cttgcctgggatctcctcctagtttcgtttcttcttctgttaggaattgtttcagcaa 480		Oy 541 ggggaagagacattgaggaccgtgttcaagaggaagccgctgcttgtggaggagtt 500 Db 1927 ggggaagaggagcattgaggaccgtgtcaagaggaagcccgctgccttgtggaagagtt 1986	Oy 601 gagaaaaccaagggtggtgaccctactccatatcactgaccttactggactactct 560 Db 1987 gagaaaaaccaagggtggtgaacatactctatcactgaccttctggactctcc 2046	Oy 661 tetetactgacattettggaaacatttcaggggtggccatatetttcattatgagt-ctg 719 	Oy 720 gttgttagctcatgtgaagcggg 743 Db 2107 gttgttagctcatgtgaagcaggg 2130	RESULT 12 US-09-488-127B-59 ; Sequence 59, Application US/09488127B	APPLICANT: Thomann, Hans-Ulrich APPLICANT: FitzGerald, Michael S. TITLE OF INVENTION: RAPID DETERMINATION OF GENE STRUCTURE TITLE OF INVENTION: USING CDNA SEQUENCE	TLE KERERGE 2709.1005-000 CURRENT APPLICATION NUMBER: US/09/488,127B CURRENT FILING DATE: 2000-01-20 NUMBER OF SEQ 1D NOS: 97	SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 59 LENGTH: 8437 TIPE: DNA OPENITSH: HOSE	CONTACT: GOIO Septens : FEATURE: : NAME/KET: misc_feature	: LOCATION: 21, 33, 35, 45, 69, 70, 87, 129, 131, 153, 162, 169, 170, 10. LOCATION: 217, 248, 448, 692, 869, 870, 871, 872, 873, 874, 875 : OTHER INFORMATION: n = A.T.C or G NAME/KEY: misc feature	: LOCATION: 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, : LOCATION: 949, 951, 1517, 2448, 2457, 2465, 2472, 2473, 2474 : OTHER INFORMATION: n = A.T.C or G : NAME/KET: misc feature	; LOCATION: 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, ; LOCATION: 2482, 2486, 2488, 2488, 2489, 2490, 2491, 2492, 2493	06, 2510, 2518, 2522.	22, 2635, 2641, 2689, 3128	. LOCATION: 3380, 3381, 3382, 3384, 3385, 3386, 3387, 3388, 3385, 3385, 3387, 3388, 3385, 3385, 5. LOCATION: 3390, 3391, 3392, 3394, 3395, 3396, 3397, 3398	; NAME/KET: misc_feature ; LOCATION: 3399, 3400, 3926, 3927, 3937, 3951, 4005, 4029, 4063, 4069. ; LOCATION: 4097, 4132, 4133, 4134, 4135, 4136, 4137, 4138, 4139 ; OTHER INFORMATION: n = A,T,C or G	. LOCATION: 4140, 4142, 4143, 4144, 4145, 4146, 4147, 4148, 4149, 1140, 4150, 4151, 4177, 4177, 4191, 4193, 4195, 4201, 4203 . OTHER INFORMATION: n = A,T,C or G	; NAME/KET: misc_feature ; ; LOCATION: 4210, 4211, 4216, 4218, 4220, 4221, 4227, 4230, 4236, 4238,

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Oy 301 tgcatgtgcctgtttcagcatctgtcttggggatgggat	RESULT 13 Sequence 97, Application US/09488127B Sequence 97, Application US/09488127B GENERAL INFORMATION: APPLICANT: Thomann, Hans-Ulrich APPLICANT: FitzGerald, Michael S. TITLE OF INVENTION: RAPID DETERMINATION OF GENE STRUCTURE FILE REFERENCE: 2709.1005-000 CURRENT APPLICATION NUMBER: US/09/488,127B CURRENT APPLICATION NUMBER: US/09/488,127B SOFTWARE: FALSE OF OF WINDOWS Version 4.0 SOFTWARE: PASTSEQ for Windows Version 4.0 TIPE: DNA TIPE: DNA ORGANISM: HOMO Sapiens FRATURE: FRATURE:		NAME/KEX: MISC_feature LOCATION: 1645, 1646, 1647, 164 LOCATION: 1655, 1656, 1657, 165 OTHER INFORMATION: n = A,T,C ox NAME/KEX: MISC_feature LOCATION: 1699, 1705, 1720, 173 LOCATION: 1819, 1862, 1937, 275 OTHER INFORMATION: n = A,T,C ox	

61 tgctaaatcaggcttagcaaatggacaaaatagtaacttcgtttgctgttatctctgtct 120 5; Gaps DB 18; Length 8437; Indels Query Match 83.8%; Score 622.6; DB 18; Best Local Similarity 93.3%; Pred. No. 9.7e-174; Matches 694; Conservative 0; Mismatches 45; 181 g С ó ò g ò ò

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US-60-182-895-148
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Sequence 147, Application US/60182895

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN:
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00262
CURRENT APPLICATION NUMBER: US/60/182,895
CURRENT APPLICATION NUMBER: US/60/182,895
SOURMER FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 590
SEQ ID NO 147
                                                                                                                                                                                                                                                                                                                                                   Length
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Pred. No. 2.2e-
0; Mismatches
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al Similarity 99.5%;
568; Conservative
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IIILE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
IIILE OF INVENTION: PROTEINS, WUCLEIC ACID MOLECULES ENC:
IIILE OF INVENTION: DRUG-METABOLIZING PROTEINS,
IIILE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLO00262
CURRENT APPLICATION NUMBER: US/60/182,895
CURRENT FILING DATE: 2000-02-16
NUMBER OF SED ID NOS: 590
SOTUMARE: FastSEQ for Windows Version 4.0
SED ID NO 148
LENGTH: 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 555.8; DB 51;
Pred. No. 2.2e-154;
0: Mismatches 2;
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ilarity 99.5%;
Conservative
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Best Local Similarity
Matches 568; Conserv
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Search completed: April 19, 2002, 11:06:25 Job time: 13485 sec
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L16881 Homo sapien

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Database

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ALI33513 Homo Sapia
ALI33513 Homo Sapia
ALI35967 Homo Sapia
ALI57835 Homo Sapia
ALI57835 Homo Sapia
ALI57835 Homo Sapia
ACO18812 Homo Sapia
ACO18812 Homo Sapia
ACO1881 Homan Cytoc
B10853 Human Cytoc
B10853 Human Cytoc
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ACO83888 Rattus no
M15331 Human 11 ver
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ACO83 Human Cytoc
ACO7931 Human Cytoc
ARO71570 Sequence
ARO71580 Sequence
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                                                                                                                                                                                                                                                                                                                                                                  M18361 Rat cytochr
293098 S.scrofa CY
293100 S.scrofa CY
                                                                                                                                                                                                                                                                                                                                                                                           M24237 Rat cytochr
D17674 Mouse mRNA
J02657 Rat cytochr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (sites)
Goldstein,J.A., Raucy,J.L., Blaisdell,J.A., Faletto,M.B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUM2C9XO5 323 bp DNA PRI 08-FI
Homo sapiens cytochrome P4502C9 (CYP2C9) gene, exon 7.
L16881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L16881.1 G1:291611
CYPE09: cytochrome P450; mephenytoin 4-hydroxylase.
5 of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                        HUMZC18X06
AL157835
AL359672
AC018872
AC013318
RABP4501
AR071576
HUMCYP2C9
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HUMCYPMP
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AC083888
HUMCYP2C17
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HUMCYPC219
E11555
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1278.330 Million cell updates/sec
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1 cocctgaattgctacaacaa.....aaattcatagtatcatttt 323
                                                 April 19, 2002, 09:32:08 ; Search time 4168.4 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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Cloning and expression of complementary DNAs for multiple members of the human cytochrome P450IIC subfamily Biochemistry 30, 3247-3255 (1991) 91182740

(bases 1 to 323)

MEDLINE REFERENCE JOURNAL

TITLE

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

08-FEB-1999

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Morais, S.M., Schweikl, H., Blaisdell, J. and Goldstein, J.A. is structure and upstream regulatory regions of human CYP2C9 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (26-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14529836.
                                                                                                                                                                                                                                                                                                                                                       121 gcatgcaagacaggagccacatgccctacacagatgctgtgtgcacgaggtccagagat 180
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AL359672.17 GI:14575223
HTG: HTGS_PHASE1: HTGS_ACTIVEFIN; HTGS_DRAFT: HTGS_FULLIOP
                                                                                               /tissue_type="liver"
/tissue_lib="EMBL3 library from J.A. Goldstein"
70. 257
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                           Biochem. Biophys. Res. Commun. 194 (1), 194-201 (1993) 93326116
                                                                                                                                                                                                                                                                Length 323;
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae:
1 (bases 1 to 143087)
Johnson.C.
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                           100.0%; Score 323; DB 9;
100.0%; Pred. No. 1.5e-84;
ive 0; Mismatches 0;
                                                                                                                                                                                                                93
                                                                                /organism~"Homo sapiens"
/db_xref~"taxon:9606"
                                                                                                                                                                                                    /evidence=experimental
                                                           Location/Qualifiers
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                                                                                                                                           /gene="CYP2C9"
                                                                                                                                                                            /citation=[1]
/number=7
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Best Local Similarity 100.
Matches 323; Conservative
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                       CYP2C18
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Gene
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AUTHORS
TITLE
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Center code: SC

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                                                                                    Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08755; 100% of reads
Sequencing vector: plasmid; L08755; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 14.2666 bases at least 040
Consensus quality: 14.2920 bases at least 030
Consensus quality: 14.2920 bases at least 020
Insert size: 14.2987; sum-of-contigs
Insert size: 14.2987; sum-of-contigs
Quality coverage: 8.55x in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47006 47105: contig of 47005 bp in length
47006 47105: gap of 100 bp
47106 143087: contig of 95982 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 others
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47106. 143087
47106. 143087
41247 a 26155 c 27788 g 47797 t
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/note="assembly_fragment:00494
                                                Center project Information
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-208C17"
Web site: http://www.sanger.ac.uk
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                         Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 173154)

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Submitted (03-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14456168.
                                  AL133513 173154 bp DNA HTG 04-JUL-2001
Homo sapiens chromosome 10 clone RP11-400G3, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.58
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 172989 bases at least 040
Consensus quality: 173136 bases at least 030
Consensus quality: 173145 bases at least 030
Consensus quality: 173145 bases at least 020
Insert size: 173154; sum-of-contigs
Insert size: 116005; 33.1% error; agarose-fp
Quality coverage: 6.48 x in 020 bases; sum-of-contigs
Quality deverage: 9.80x in 020 bases; agarose-fp
                                                                                          AL133513.11 GI:14575067
HTG: HTGS_PHASE2: HTGS_ACTIVEFIN: HTGS_DRAFT: HTGS_FULLTOP.
human.
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

1. 173154
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32272 c 33707 g 58012 t
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92.6%; Pred. No. 3.4e
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-400G3"
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1. .173154
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                                                                                                                                                       Homo sapiens
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Best Local Similarity
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                                                                                     AL133513
                                                                                                                                                                                                                       Brown, J.
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Mashreghi-Mohamadi, M.

Direct Submission
L Submitted (11-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (11-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk
On Jun 14, 2001 this sequence version replaced gi:14148873.
Center: Sanger Center
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Catarrhini; Hominidae; Homo.
Homo sapiens chromosome 10 clone RP11-466J14, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: XARP4: version 4.5
Assembly program: XARP4: version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 205236 bases at least Q40
Consensus quality: 205540 bases at least Q30
Consensus quality: 205560 bases at least Q20
Insert size: 205691; sum-of-contigs
Insert size: 188405; 9.1% error; agarose-fp
Ouality coverage: 11.31x in Q20 bases; sum-of-contigs Quality
coverage: 12.57x in Q20 bases; agarose-fp
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HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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88341 205791: contig of 117451 bp in length.
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Mammalia; Eutheria; Primates;
1 (bases 1 to 205791)
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de Morais, S.M., Schweikl, H., Blaisdell, J. and Goldstein, J.A.

Gene structure and upstream regulatory regions of human CYP2C5 and
                                                                                                                                                                                 Db 164775 CCCTGAATIGCTAGAACAAATGTICCATITCTCTCCTCTTTTCCATCATCTTGTG 154834
                                                                                                                                                                                                                           Cloning and expression of complementary DNAs for multiple members of the human cytochrome P450IIC subfamily Biochemistry 30, 3247-3255 (1991) 91182740
                                                                                                                                                                                                                                                                                                                           164954
                                                                                                                                                                                                                                                                                                                                                                                                                        Db 165015 ACTACCTCATTCCCAAGGTAAGTTTGTCTCCTACACTCCATGTTCTTTTAIT 165074
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                       Homo sapiens (library: EMBL3 library from J.A. Goldstein) liver
                                                                                                                                                 Gaps
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Correction: Cloning and expression of complementary CDNAs for multiple members of the human cytochrome P450IIC subfamily Biochemistry 32, 1390-1390 (1993)
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Goldstein,J.A., Raucy,J.L., Blaisdell,J.A., Faletto,M.B. and
                                                                                                                                                                      1 ccctgaattgctacaacaaatgtgccatttttctccttttccatcagttttacttgg
                                                                                                                                                                                                                                                                                                                                                                                                          241 actatctcattcccaaggtaagtttgtttctcctacactgcaactccatgttttcgaagt
                                                                                                                DB 2; Length 205791;
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Homo sapiens cytochrome P4502C18 (CYP2C18) gene, exon 7.
L16874
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Romkes.M., Faletto,M.B., Blaisdell,J.A., Raucy,J.L. and
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CYP2C18; cytochrome P450; mephenytoin 4-hydroxylase.
6 of 8
                                                          100 others
                                                                                                            Query Match
Best Local Similarity 92.6%; Pred. No. 3.4e-70;
Matches 300; Conservative 0; Mismatches 23; Indels
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38262 c 40890 g 69845 t
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/organism="Homo sapiens"
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Homo sapiens
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Direct Submission
Submitted (05-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, WK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul B, 2001 this sequence version replaced gi:14586042.
                                                                                                                                                                                                                                                                                                                                                                                    242
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Homo sapiens chromosome 10 clone RP11-361K9, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                             Length 348;
                                                                                                                                                                                                                                                                                              Indels
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Best Local Similarity 91.7%; Pred. No. 7.2e-67;
Matches 289; Conservative 0; Mismatches 25
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Web site: http://www.sanger.ac.uk
                                                                                                                                                                         /evidence=experimental
/db_xref~"taxon:9606"
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AL157835.9 GI:14626943
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clone_end:SP6
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Vararyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ttatcagctaaagtccaggaagagattgaacgtgtgattggcagaaaccggagccctgc 122
Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 156104 bases at least 040 Consensus quality: 156104 bases at least 030 Consensus quality: 156216 bases at least 030 Insert size: 156492; sum-of-contigs consensus graphy: 137% error; agarose-fp Quality coverage: 8.34x in 020 bases; sum-of-contigs Quality coverage: 9.69x in 020 bases; agarose-fp
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                                                                                                                                                • NOTE: This is a 'working draft' sequence.
• This sequence will be replaced
• by the finished sequence as soon as it is
• the accession number will be preserved.
• Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
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91.7%; Pred. No. 1.3e-66;
live 0; Mismatches 25
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                                                                                                                                                                                                                                                                 Assembly program: XGA44; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 142666 bases at least Q40
Consensus quality: 142843 bases at least Q40
Consensus quality: 142843 bases at least Q30
Consensus quality: 142920 bases at least Q20
Insert size: 142920 san-of-contigs
Insert size: 156404; agarose-fp
Quality coverage: 8.5% in Q20 bases; sum-of-contigs Quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as 'This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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47106 143087: contig of 95982 bp in length.
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Best Local Similarity 83.2%; Pred. No. 1.2e-54;
Matches 253; Conservative 0; Mismatches 51;
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47106. 143087
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1. 47005
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                                                                                                                                                                                  Contact: humquery@sanger.ac.uk
                                                                                                                                                         Web site: http://www.sanger.ac.uk
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g of 12178 bp in length
f unknown length
g of 9855 bp in length
f unknown length
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length
bp in length
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30172. .35416
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="2"

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Submitted (21-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Feb 18, 2001 this sequence version replaced gi:8954228.
                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201340)
Waterston, R. H.
Db 18016 CTACCTCATCCCCAAGGTAAGCTTGTTTCTCTTACACTATATTTCTGTACTTCTGAAATT 17957
                                                                                                                   Homo saplens chromosome 2 clone RP11-140M22, WORKING DRAFT SEQUENCE, 28 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center
Center code: WUGSC
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egap of unknown length

contig of 2776 bp in length

gap of unknown length

contig of 1807 bp in length

gap of unknown length
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1502: gap of unknown length
2841: contig of 1339 bp in length
2941: gap of unknown length
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REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS

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Homo sapiens
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2 clone RP11-358N5 map 2, WORKING DRAFT
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Homo sapiens chromosome 2 clone
SEQUENCE, 22 unordered pieces.
AC013318 5 01:10280844
HTG; HTGS_PHASE1; HTGS_DRAFT.
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99 24398: gap of 100 bp
99 29876: contig of 5478 bp in length
77 29976: app of 100 bp
77 36607: contig of 6631 bp in length
88 36707: gap of 100 bp
8 43142: contig of 6435 bp in length
13 4342: gap of 100 bp
13 49210: contig of 5968 bp in length
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Rabbit cytochrome P450IIC5 (CYP2C5) gene, exon 7.
M74204.1 G1:165568
Cytochrome P450 IIC5; drug metabolism; microsomal membrane protein; monooxygenase.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
H (bases 1 to 595)
Zhao, J., Chan, G., Govind, S., Bell, P. and Kemper, B.W.
Structure of 5' regions and expression of phenobarbital-inducible abbit cytochrome P450IIC genes
DNA Cell Biol. 9, 37-48 (1990)
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                                                                                                                                                                                                                        Length 210821;
                                                                                                                                                                2111 others
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                    64.6%; Score 208.8; DB 2;
ilarity 82.5%; Pred. No. 1.3e-50;
Conservative 0; Mismatches 52;
                                                                                                                                               vector_side:right"
37637 c 36968 g 66777 t
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/organisma.oryctolagus cunicn
/strain="New Zealand White"
/db_xref="taxon:9986"
/cell_type="hepatocyte"
/tissue_type="liver"
/dev_stage="adult"
/germline
162. .349
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140060. .155880
/note-'assembly_fragment"
15981. .170719
/note-'assembly_fragment"
170820. .200316
/note-'assembly_fragment"
200617. .210821
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                                                                                                                                   clone_end:T7
                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                             67328
                misc_feature
                                            misc_feature
                                                                        misc_feature
                                                                                                                                                                                                                                                Matches 264;
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Best Local
                                                                                                                                                           BASE COUNT
ORIGIN
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ORGANISM
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Query Match
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                  RESULT 12
HUMCYP2C9
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                                       DEFINITION
                                                                             ORGANISM
                                                                                                                                                                                                                            BASE COUNT
ORIGIN
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E10631
                                                ACCESSION
                                                      VERSION
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                                                                                                    REFERENCE
                                                                                                            AUTHORS
                                                                                                                                                         MEDLINE
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                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1854)
Goldstein,J.A. and De Morais,S.M.F.
Clouind, expression and diagnosis of human cytochrome P450 2C19:
the principal determinant of s-mephenytoin metabolism
Patent: US 5912120-A 4 15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 tettatcagetaaagtecaggaagagttgaacgtgtgattggcagaaaccggageeet 120
                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  59.4%; Score 192; DB 6; Length 1854; 100.0%; Pred. No. 7.3e-46; Live 0; Mismatches 0; Indels
                                                      Length 595;
                                                                   55; Indels
                                                                                                                                                                                                                                                                PAT
                                                    Score 194; DB 4;
Pred. No. 1.7e-46;
0; Mismatches 55
                      195
                                                                                                                                                                                                                                                                                                                                                                                      536
                                                                                                                                                                                                                                                         AR071576 1854 bp DNA
Sequence 4 from patent US 5912120.
AR071576
              /evidence-experimental
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              /organism="unknown"
                       δ
                                                                                                                                                                                                                                                                                                                                                                                      381 g
                      110
/gene="CYP2C5"
/number=7
                                                                                                                                                                                                                                                                                    AR071576.1 GI:7222464
                                                   Ouery Match 60.1%;
Best Local Similarity 81.0%;
Matches 23%; Conservative
                      130 c
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                                                                                                                                                                                                                                                                                                                                                                     .1854
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Best Local Similarity 100.
Matches 192; Conservative
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                                                                                                                                                                                                                                                                                                           Unknown.
Unclassified.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ tbases 1 to 1854)
Romkes,M., Faletto,M.B., Blaisdell,J.A., Raucy,J.L. and Goldstein,J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning and expression of complementary DNAs for multiple members of the human cytochrome P450IIC subfamily [published erratum appears in Biochemistry 1993 Feb 9;32(5):1390]
Biochemistry 30 (13), 3247-3255 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                25.
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100.0%; Pred. No. 7.3e-46;
iive 0; Mismatches 0;
Human cytochrome P4502C9 (CYP2C9) mRNA, M61855 J05326 CM61855 J GI:181301 CYtochrome Cyt
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                                                                                                                                                                                  cytochrome P450; cytochrome P450 2C9 Human, cDNA to mRNA. Homo sapiens
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02-SEP-2000 (Rel. 65, Last updated, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/gene="CYP2C9"
a 424 c 38
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13. .1485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 192; Conserv
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H., Nakatsuka I.;

208279,

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Homo sapiens
Sukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1814)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohgiya, S., Komori, M., Ohi, H., Shiramatsu, K., Shinriki, N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $46963 1814 bp mRNA PRI 0:
putative CYPC2C9 gene [human, liver, mRNA, 1814 nt]
$46963.1 GI:258514
                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 58.9%; Score 190.4; DB 22; Length Best Local Similarity 99.5%; Pred. No. 2.1e-45; Matches 191; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                  /product="human cytochrome P450 2C9"
                                                                                                                    15-JUL-1994 JP 1994164184
20-JUL-1993 JP 93P 201120, 30-JUL-1993 JP 93P 2
17-JUN-1994 JP 94P 136053
HAYASHI KOJI, SAKAKI TOSHIVUKI, YABUSAKI YOSHIYASU, KOMAI KOICHIRO, NAKATSUKI IWAO
C1201/02.c1ZM1/34.C1201/26;
strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                BP; 413 A; 345 C; 319 G; 396 T; 0 other;
                                       Hayashi K., Sakaki T., Yabusaki Y., Komai K., Kaneko
*METHOD POD EVALUATING SAFETY*;
Patent number JP1996556695-A/2, 05-MAR-1996.
SUMITOMO CHEM CO LTD.
  Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                       1. .1473
                                                                                         Homo sapiens (human)
JP 1996056695-A/2
05-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1139 TCATTCCCAAGG 1150
                                                                                                                                                                                                    topology: Linear;
hypothetical: No;
                                                                                                                                                                                                                         anti-sense: No;
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AUTHORS
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KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                          127 aagacaggagccacatgccctacacagatgctgtggtgcacgaggtccagagataccttg 186
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                         FUNAE YOSHIHIKO, IMAOKA SUSUMU, MATSUKI YASUSHI, HAYASHI KOJI.
                                                                                                                   YABUSAKI YOSHIYASU
CO7K16/18, C12N15/09, G01N33/53, G01N33/53//C12N1/19, C12N9/02,
(C12N1/19,
                                                                                                                                                                                                                                                                                                                                                     Length 1473;
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                  Funae I., Imaoka S., Matsuki Y., Hayashi K., Yabusaki Y.;
"AMTIBODY RECOGNIZING CYTOCHROME P4502C9 ORIGINATED FROM MAN";
Patent number JP1996027196-A/5, 30-JAN-1996.
SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                  58.9%; Score 190.4; DB 22; Length 99.5%; Pred. No. 2.1e-45; Ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                       Sequence 1473 BP; 413 A; 345 C; 319 G; 396 T; 0 other;
                                                                                                                                                                                                                                         /product "cytochrome P4502C9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2)
                                                                                                                                                                                                         /organism="Homo sapiens"
/tissue_type="liver"
1.1473
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02-SEP-2000 (Rel. 65, Last updated, Version

    1473
    db_xref="taxon:9606"
    /organism="Homo sapiens"

                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; RNA; HUM; 1473 BP.
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding human cytochrome P450
                                                                                                 13-JUL-1994 JP 1994161551
                                                                                                                                                                                                    1. .1473
                                                                                                                                                           strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                  Query Match 58.9
Best Local Similarity 99.5
Matches 191; Conservative
                                                                     sapiens (human)
                                                                            JP 1996027196-A/5
30-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1139 TCATTCCCAAGG 1150
                                                                                                                                                                       topology: Linear;
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                                                                                                                                                C12R1:865);
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1-1473
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E10853
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Gaps

.; 0

DB 22; Length 1473;

05-AUG-1999

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/ gene="putative CYPC2C9 gene"
//note="This sequence comes from Fig. 1"
//note="This sequence comes from Fig. 1"
//roduct="cytochrome P-450"
//product="cytochrome P-450"
//protein_id="AAB23864.2"
//db_xxef="G1:5705937"
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PCNVICSIFFHKREDVKOOFLULMERLINNNIKILSSPWIDICNNFSPIIDYFPGTHN
KLLKNVAFMKSYILEKVKEHOESMDNNNPQDFIDCTLMKMEKEKHNPOSEFTIESLEN
TAVDLEGAGTETTSTTLRYALLLLKHPEVTAKVOGEIERVIGRNSFPCMPORTDAVHEVORYIDLLPTSTLLKHPEVTAKVOGEIERVIGRNSFPCMPF
TDAVVHEVORYIDLLPTSTLLKHPEVTAKVOGEIERVIGRNSFPNPE
MFDPHHFLDEGGNFKKSKYFMPFSACRICVGEALAGMELFLETSTLUNFUKSLVD
PRINDITPVNGRESNPPFVOLCFILV"
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Ramataki,T.
Six-base deletion occurring in messages of human cytochrome P-450
in the CYP2C subfamily results in reduction of tolbutamide
                                                                                                                    GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 117179] from the original journal article. This sequence comes from Fig. 1.

Author also gives sequence for another cytochrome P-450 that contains a 6-base deletion of nucleotides 783-788.
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Best Local Similarity 99.5%; Pred. No. 2.2e-45;
Matches 191; Conservative 0; Mismatches 1: Indels 0;
                                                                                                                                                                                                                                                    1. 1814
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. 1814
/gene="putative CYPC2C9 gene"
3. 1436
                                                              hydroxylase activity
Blochem. Int. 27 (6), 1073-1081 (1992)
93075249
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Sequence 5, Appl 1
Sequence 3, Appl 1
Sequence 17, Appl 1
Sequence 17, Appl 1
Sequence 22, Appl 2
Sequence 24, Appl 2
Sequence 26, Appl 2
Sequence 21, Appl 2
Sequence 21, Appl 2
Sequence 21, Appl 2
Sequence 22, Appl 2
Sequence 24, Appl 2
Sequence 15, Appl 3
Sequence 16, Appl 3
Sequence 17, Appl 3
Sequence
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APPLICANT: GOLDSTEIN, Joyce A.
MURGER OF INVENTION: SUBFAHLY
WORRESPONDER OF SUBFAHLY
ADDRESSE: TOANSEND AND CONTRIBUTE OF STREET:
ADDRESSE: TOANSEND AND CONTRIBUTE OF STREET OF STR
                                                                                                               US-08-750-701-1
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US-08-145-658D-14
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April 19, 2002, 08:10:39 ; Search time 130.44 Seconds (without alignments) 560.813 Million cell updates/sec
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5: /cgn2_6/ptodats_7/lins/fb_COMB.seq:*

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6: /cgn2_6/ptodats_Regiser

7: /cgn2_6/ptodats_Regiser

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Ouery Match 59.4%; Score 192; DB 2; Length 1854; Best Local Similarity 100.0%; Pred. No. 2.1e-51; Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps
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SEGREAL ALTEROMATION:

APPLICATE TO MUSES-SPARS, NATION:

APPLICATE TO MUSES-SPARS, NATION:

APPLICATE TO MUSES-SPARS, NATION:

APPLICATE TO THE STATION:

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ANDRESSES:

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Db 1091 ACCTTCTCCCACCAGCCTGCCCATGAGTGAGTTAAATTCAGAAACTATC 1150
OY 247 tcattcccaaqqq 258
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OTHER IMPOBATION: /note- "Corresponds to positions -12 to-1
05-08-238-8218-611-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICAMT: GOLISTEIN, JOYCE A.
APPLICAMT: GOLISTEIN, JOYCE A.
APPLICAMT: GOLISTEIN, JOYCE A.
APPLICAMT: DE MORES-SENES, MATJOTE
APPLICAMT: DE MORES-SENES, MATJOTE
TITLE OF INVENTION: CTTOCHEOLE P450 2C19: THE PRINCIF
TITLE OF INVENTION: CTTOCHEOLE P450 2C19: THE PRINCIF
MINDRER OF SEQUENCES: 61
CORRESPONDENCE ALDRESS:
ADDRESS-CONDENCE ALDRESS:
ADDRESS-CONDENCE ALDRESS:
CONTROL CALLOR OF TRANSLES OF STREET: TWO EMBACRACHO CENTER, 8th Floor
STATE: CALIGORIA A.
CONTROL STREET: TWO EMBACRACHO CENTER, 8th Floor
STATE: CALIGORIA A.
CONTROL STREET: PC-DOS/AS-DOS
STATE: CALIGORIA A.
CONTROL REPORTED READER PORT:
CONTROL STATES AND DATA:
APPLICATION BATH:
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ANDRESS-CONTROL A.
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Sequence 4, Application US/08238821B
Patent Mo. 5912120
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APPLICANT: GOLDSTEIN, JOYCE A.

FITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY

TITLE OF INVENTION: SUBFAULT REAGES OF THE HUMAN CTTOX

MINERS OF SUPPLY SUBFAULT

MERCHANDERS OF SUPPLY SUBFAULT

ANDRESSE: Townsend and Townsend Khourle and Crew

STREET: 39 LYLLON AVENUE FORM:

ANDRESSE: Townsend and Townsend Khourle and Crew

STREET: 39 LYLLON AVENUE FORM:

ANDRESSE: Townsend and Townsend Khourle and Crew

STREET: 39 LYLLON AVENUE FORM:

ANDRESSE: Townsend and Townsend Khourle and Crew

STREET: 39 LYLLON AVENUE FORM:

ANDRESTEER: Floppy disk

COMENTER: His PC Compatible

SOFTHAME: Patentin Release 11.0, Version 11.25

APPLICATION HORSE: 15.3094

APPLICATION HORSE: 15.3094

APPLICATION HORSE: 37.505

REPRESENCE/POCKET HORBER: 15.300

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Best Local Similarity 99.54; Pred. No. 6.8e-51;
                                                                           Query Match 59.4%; Score 192; DB 5; Length 1854; Best Local Similarity 100.0%; Pred. No. 2.1e-51; Matches 192; Conservative 0; Mismatches 0; Indels
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US-08-201-118-10
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LOCATION: 1..10
OTHER INFORMATION: /note- "Corresponds
OTHER INFORMATION: for 65 of Figure 2."
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US-08-238-821B-10

: MOLECULE TYPE: CDNA PCT-US95-05744-10

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Local Stalinity 99.9; Score 190.4; DB 2; Length 1952;

Matches 191; Conservative 0; Misatches 1; Indels 0; Caps 0;

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SECURCE 14. APPLICATION US/08201118

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        Ouery Match 55.91, Score 180.6, OB 1; Length 1892;
Best Local Similarity 95.31, Pred. No. 8.7e-48;
Watches 183; Conservative 0; Mismatches 9; Indels 0; Gaps
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Db 1025 Accitciccccaccagoccgatgacctgtgacattaaatcagaaactatc 246

Db 1025 Accitcicccaccaccacccccafaccagaacctgacctaractatcagaaactatc 1084

Oy 247 tcattcccaaga 258
                                                                                                                     Onery Match 58.5%; Score 188.8; DB 2; Length 1419; Best Local Similarity 99.0%; Pred. No. 26-50; No. 26-50; Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps
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S8.51, Score 188.8; DB 2; Length 1591;
Best Local Statistity 99.01, Pred. No. 21e-50;
Natches 199; Conservative 0; Mismatches 2; Indets 0;
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PSequence 1, Application 05/08194981E

PREMER NO. 5886137

GENERAL HOPMANTON:

APPLICANT CURRIERICL. P. Peter

APPLICANT CURRIERIC. P. Peter

APPLICANT CILLAN. 211abbeth N. J.

ITHER OF INVENTION: CUTCHROME P450

NORRESPONDENCE: 68

CORRESPONDENCE: 68

CORRESPONDENCE: 100 CUTCHROME P450

NORRESPONDENCE: 100 CUTCHROME P450

STRTES. SULTE 1200, 127 Peachtree Street, NE

CITT: ALIANA

STRAIL GONDENCE: 68

COMPUTER REALABLE PORN:

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COMPUTER REALABLE PORN:

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APPLICATION NORS: 38 298

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Matches 183; Conservative
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Sequence 14, Application US/08238821B
Patent No. 5912120
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MOLECULE TYPE: DNA (genomic)
HTPOTHETICAL: YES
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 Query Match
 55:91;
 Score 180.6;
 DB 2;
 Length 1892;

 Best Local Similarity
 95.31;
 Pred. No. 8.7e-48;

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0; Gaps
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APPLICANT: GOLDSTEIN, Joyce A. APPLICANT: GENERALS: SAGIA M.F.

TITLE OF INVENTION: CUTTOCHROWE PASO 2C19: THE PRINCIPAL ITILE OF INVENTION: OF S-MEPHINTOIN METABOLISH GORRESCHEERS: JOYCHORSEN GORDSTEIN: JOYCHORSEN GORDSTEIN: JOYCHORSEN GORDSTEIN: JOYCHORSEN GORDSTEIN: GOLDSTEIN: JOYCHORSEN GORDSTEIN: GOLDSTEIN: GOLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Sequence 2, Application US/08201118
: Sequence 2, Application US/08201118
: GENERAL INFORMATION:
: APPLICART: GOLDSTEIN, JOYCE A.
: APPLICART: GOLDSTEIN, JOYCE A.
: TITLE OF INVERTION: CLONING AND EXPRESSION OF CONFLENENTRY:
: TITLE OF INVERTION: SUBPARITY
: TITLE OF INVERTION: SUBPARITY
: MADRESSES: Townsend and Townsend Khourie and Crev
: STREET: PAIO AILO
: GOTTH: PAIO AILO
: GOTTH: US
: CONFIRME US
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US-08-201-118-2
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US-06-218-6118-2

US-06-218-6118-2

US-06-218-6118-2

GENERAL INFORMATION:

APPLICANT: ROMES-SPARK, MATJOTIE

APPLICANT: ROMES-SPARK, MATJOTIE

ITILE OF INVENTION: CLOMIN, EXPRESSION AND DIAGNOSIS OF HUAN

ITILE OF INVENTION: CLOMIN, EXPRESSION AND DIAGNOSIS OF HUAN

ITILE OF INVENTION: CLOMIN, EXPRESSION AND DIAGNOSIS OF HUAN

ITILE OF INVENTION: CLOMIN, REPHENTION METABOLISH

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Obsery Match 55.09; Score 177 6; DB 1; Length 1746; Best Local Similarity 95.31; Pred: No. 7.5e-47. Matches 183; Conservative 0; Mismatches 9; Indels 0; Gaps 67 cagctaaagtccaggaagaattgaacgtgtgattggcagaaaccggagccctgcatgc 126

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Ouery Match 55.0%; Score 177.6; DB 5; Length 1746; Best Local Similarity 95.3%; Pred. No. 7.5e-47; Matches 183; Conservative 0; Mismatches 9; Indels 0;
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Best Local Similarity 92.21; Pred. No. 8.7e-44;
Matches 177; Conservative 0; Mismatches 15; Indels 0
                                                                                                                                                                                                                                                                                                                                                               Ouery Match 55.0%: Score 177.6; DB 2; Length 1746; Best Local Similarity 95.3%; Pred. No. 7.5e-47; Matches 183; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-1059-05144.
Sequence 2. Application PC/TUS9505144
GENERAL IMPORATION:
APLICANT: GOLGSPEIN. Joyce A.
APLICANT: GOLGSPEIN. JOYCE A.
APLICANT: DE MORALS. SOALA H.
APLICANT: GOLGSPEIN. MATJOTIC
APPLICANT: GOLGSPEIN. GOLGSPEIN. MUNGES OF STREET: 319 LYTCO Avenue
COTRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AVENUE
STREET: 319 LYTCO Avenue
COTRESSOURMER: ALIGORIA Avenue
COTRESSOURMER: ALIGORIA Avenue
CONFORTE: LIMP ACCORDALIA COMPALIA
COMPUTER: IMP COMPALIA
COMPUTER: IMP COMPALIA
COMPUTER: TAPPRICATION AVENUE
COMPUTER: PAPPRICATION MAT.
APPLICATION MUNGER: US 08/201,118
FILLED DATE: 06-MAT-1994
PRIOR APPLICATION DATA:
APPLICATION MUNGER: US 08/201,118
FILLED DATE: 06-MAT-1994
PRIOR APPLICATION MATA.
APPLICATION MUNGER: US 08/201,118
FILLED DATE: 06-MAT-1994
PRIOR APPLICATION DATA:
APPLICATION MUNGER: US 08/201,118
FILLED DATE: 06-MAT-1994
RESPERENCE OF AVENUE : 180 1/280-192-1-1
TELEPROMER: ALIGNED HANDER: 180 1/280-192-1-1
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TELEPROMER: ALIGNED HANDER: 180 1/280-192-1-1
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GREEKEAL INCOMENTIN, JOYCE A. A. PEDLICARTY GOLDSTEIN, GOLDST
                                                                                                               Oy 127 aagacagagccacatgccctacacagatgctgtggtgcacgaggtccagagataccttg 186 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 |
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Search completed: April 19, 2002, 08:10:43 Job time: 2943 sec

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Cytochrome P450 2C	E		/*tag- f

SUMMARIES

Page 2

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between regions of nucleic acids that were separated by intervening sequence, and also for determining boundaries present in genes containing group 1 type introns such as Tetrahymena FRNA, where self-splicing occurs in the presence of guantonism cofactor. The present sequence is human cycochrome P450 (F79450) A219 gene related to the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CYP2CB related DNA containing a biallelic polymorphism SEQ ID 51
                                                                                                                                                               Ouery Watch 85.74: Score 276.8; DB 22; Length 8437; Best Local Similarity 92.94; Pred. No. 6.4e-79; Matches 301; Conservative 0: Mismatches 22; Indels 1; Gaps
                                                                                                            Sequence 8437 BP; 2392 A; 1501 C; 1541 G; 2654 T; 349 other;
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                              *Primer
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. ให้เป็นเพลาน เรื่องโดย น้ำไม่รักแล้ว ในเป็น

Human; biallelic marker; single nuclectide polymorphism; SNP; MGSTII; microsomal gutathlone Stransterase II; malate decarboxylase enzyme. DMEI; MEI; cytochrome P450; glutethlone reductase; GSHR; GSHS; GGT5; dlearin-containing monoxygenase; FNP; gamma-glutamyltransferase 5; dlepetidase; DP; glucose 6-phosphate dehydrogenase; G6P0B; haplotype; phosphodluconate dehydrogense; PCDH; darmy metabolism; phenotype; uridine dlaposphate glucoronosyl transferase; UGT2; asthma; hepatoxicity; ziteuton; ds. Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine | MARSING | A. A. MARSING | MARSING

The present invention relates to a method for determining gene structure when the general sequencies using when the general sequencing the gene across exon-intron boundaries using evenly spaced persents or tiled primers or tiled primers comprises uncleic acids that hybridise to the known coNA sequence of the gene at about 100:300 base intervals and the gene comprises the template. Gene structure can be determined without the need to sequence the entire gene. The method provides information necessary to determine gene structure and phenotypic expression without the need to sequence entire chronosomal ropy of the gene or fragment. The methods are useful in germline sequence variation analysis. The method is also useful for determining the boundaries

Cytochrome P450 2C19; human; liver; PCR; primer; detection; CYP2C19; stereospecific S-mephenytoin 4'-hydroxylase activity; polymorphism; ss.

Homo sapiens.

Cytochrome P450 2C9 clone 25 coding sequence.

CDS 13..1485
CDS /*tag* a

/*tag* a

misc_difference 1087

/*tag- b /note- "variable position"

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Sequences news...

biallelic markers. The sequences are travers. If (MSTII), malater it clicitating microscans glutathinose S-transferase II (MSTII), malater decarboxylase enzyme (DMI-NEI), cytochrome p450, glutathione created grammage (GSR-NEI). Cytochrome p450, glutathione created compared (GSR-NEIS). If latin containing monoxyptenases (FMD).

Semence and compared (GSR-NEIS). [latin containing monoxyptenases (FMD).

Contains a biallelic marker/polymorphism, which is represented in the sequence as a degenerate-undefined base. The genes of which the biallelic marker containing sequences are related are involved in drug metabolism. Containing sequences are related are involved in drug metabolism. Containing sequences are related are involved in drug metabolism. Containing sequences are related are involved in drug metabolism. Containing in chief and four alternative MSTII cohe sequences. AMSTIGO research in the marker in the semantic sequences. AMSTIGO are used in an example for the amplification of human genomic DNA fragments. The content of a mucleotide at a DNE- or MSTII-related bialielic marker in comparation of an allele of a DNE- or MSTI-related bialielic marker and containing the deficient and allele of a DNE- or MSTI-related bialielic marker and containing the papalation of an allele of a DNE- or MSTI-related bialielic marker and containing the containing training the deficient of a distribution of a dis
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or is at risk of developing hepatoxicity on treatment with
                                   Polynucleotides comprising sequences from malate decarboxylase enzyme.related biallelic markers used for genotyping
                                                                                                                                            Claim 13; Page 281; 673pp; English.
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Sequence 1001 BP; 270 A; 166 C; 178 G; 384 T; 3 other;

New isolated cytochrome P450 2C subfamily member identifying drugs metabolised by S-mephenytoin 4' activity and to develop other screening assays

Example 2; Page 95-96; 169pp; English.

De Morais SMF, Goldstein JA, Romkes-Sparks M;

WPI; 1996-077257/08. P-PSDB; AAR89862.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

08-MAY-1995; 95WO-US05744. 06-MAY-1994; 94US-0238B21.

W09530766-A1. 16-NOV-1995.

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242 ctatotoattocoaaggtaagtttgtttetoctacactgcaactocatgttttcgaagtc 301
bear Local Stallarity 69.01: Score 223; DB 21: Length 1001; Bear Local Stallarity 63.01; Pred. No. 5.18-62; Metches 15: Conservative 1: Mismatches 51; Indels 0:
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127 aagacaggagccacatgcctacacagatgctgtggtgcacgaggtccagagataccttg 186
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Best Local Similarity 100.0%; Pred. No. 7.3e-7.0;
Matches 192; Conservative 0; Hismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                 Sequence 1854 BP; 513 A; 424 C; 381 G; 536 T; 0 other;
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AAT11378 standard; cDNA; 1854

09-SEP-1996 (first entry)

AAT11378; RESULT 3 AAT11378 1D AAT11 XX AAT11 XX AAT11 XX 09-SI sasabinen halmalia

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The present sequence encodes a fusion proteins comprising a portion of a abacterial cytochrome P450 protein and also a portion of a mammalian cytochrome P450 protein. The fusion protein can oxidise hydrocarbons or any compound having a carbon-hydrogen bond. The fusion protein can be used for hydroxylating a compound to be oxidised. It can also be used in the bioremediation of an environmental pollutant. Since the fusion protein is soluble, it can be subject to structural elucidation proystallography for designing functional proteins. It can be readily expressed in soil bacteria to facilitate bioremediation.
                        Bacterial and mammalian chimeric cytochrome P450 protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New P450 fusion proteins - comprising a portion of a bacterial cytochrome P450 protein and a portion of a mammalian cytochrome P450 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial; mammalian; cytochrome P450; chimeric; fusion protein; oxidise; hydrocarbo; carbon hydrogen boad; hydroxylating; bloremediation; environmental pollutant; ss.
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                                                                                                                                                                                                                                                                                                                                                                                    AAX19916 standard; DNA; 1356 BP.
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P-PSDB; AAY04126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX19916;
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MAX199
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1031 magacaggagccacatgccctacacagatgctgtggtgcacgaggtccagagataccttg 1090
                                                          Screening for drugs metabolised by cytochrome P450 - for identifying mutagenic, carcinogenic, or cytotoxic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cochrome P450; drug screening; S-mephenytoin 4'-hydroxylase;
identification; autaente; carcinogenie; cytotoxie; haemoprotein;
xenobiolite; environmental poliutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cytochrome P450 2C9 clone 25 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV44154 standard; cDNA; 1854 BP
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09-APR-1992; 92US-0864962.
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                                                                                                                                                                                                                                                                                                                                                                                                   MAY4154

ANV4154

ANV
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Oucry Match 58.9; Score 190.4; DB 20; Length 1356; Best Local Similarity 99.3; Pred: No. 2.18-51; Indels 0; Gaps Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps
Sequence 1356 BP; 349 A; 386 C; 323 G; 298 T; 0 other;
                                                                    8 & 8 & 8
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8 8 5

Oubery Match 59.4%; Score 122; DB 19; Length 1854; Best Local Similarity 100.0%; Pred. No. 7.38-55; Matches 3192; Conservative 0; Mismatches 0; Indels 0; Gaps

Sequence 1854 BP; 513 A; 424 C; 381 G; 536 T; 0 other;

187 accttctccccaccagcctgccccatgcagtgacctgtgacattaaattcagaaactatc 246

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MOD Apr 22 U8:41:46 2002
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The nucleotide sequence of the CDNA encoding the human cytochrome P450

Steedes ACS. The gene encodes a protein of 491 amino acids. The CDNA

vas amplified by PCR using the primers AA087735-8. The product was

Clouded into the yeast expression vectors PAM310 or PAMRR to produce the

vervors p2C9 for the expression of the cytochrome P450 alone or p2C9R

Compound by reacting the chemical compound with recombinantly produced

The vectors are used in a method for evaluating the safety of a chemical

Compound by reacting the chemical compound with recombinantly produced

(AA087718) or AM (AA087717), or their autiliary species and variants

C. (AA087718) or and yeast NADPP P450 reductase, either as a fused protein

or in cell erracts, and manipsing the resulting metabolite to assess the

safety of the chemical compound. The metbod is useful for determining

whether the chamical compound. The metbod is useful for determining

whether the chamical compound. The metabolite, will be converted into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buman cytochrome P450; amplification; PCR; primer: expression vector;
yeast RADPH-P450 reductase; safety; fusion protein; metabolite:
carcinogen; mutagen; liver metabolism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi K, Kaneko H, Komai K, Nakatsuka I, Sakaki T;
Yabusaki I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1473 BP; 413 A; 345 C; 319 G; 396 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cytochrome P450 molecular species 2C9 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Examples; Page 23-25; 124pp; English.
                                                                                                                                                                                                                                                   AAQ87715 standard; cDNA; 1473 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HATA/) HAYASHI K.
(SUND ) SUMITOMO CHEM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1993; 93JP-0180246.
20-JUL-1993; 93JP-0201120.
30-JUL-1993; 93JP-0208279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94EP-0111298.
                                                                                                                                                                                                                                                                                                                                                                                        10-MOV-1995 (first entry)
WPI; 1995-116991/16.
P-PSDB; AAR72361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP644267-A.
                                                                                                                                                                                                                                                                                                                     AAQ87715;
                                                                                                                                                                                | MAN | MAN
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Ouery Match 58.9%; Score 190.4; DB 16; Length 1473; Best Local Similarity 99.5%; Pred. No. 2.2e-2; Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps

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Human cytochrome P450: amplified; PCR: polymerase chain reaction; primer; luter; yeast; expression vector; NADBH-P450 reductase; ADH gene promoter; evaluation; safety; fusion protein; metabolite; detoxification; carcinogenic; ds. Nevel method for the evaluation of the safety of a cpd. - using a human ortochrome P405 and yeast NADBH reductes to determine whether the analyte opf. is detoxified or metabolised to a cartinogen Human cytochrome P450 molecular species 2C9 gene. Example 1; Page 20-22; 74pp; Japanese. AAT28381 standard; DNA; 1473 (SUMO) SUMITOMO CHEM CO LTD. 17-JUN-1994; 94JP-0136053. 20-JUL-1993; 93JP-0201120. 30-JUL-1993; 93JP-0208279. 15-JUL-1994; 94JP-0164184. 11-OCT-1996 (first entry) WPI; 1996-182311/19. P-PSDB; AAR93168. Homo saplens. JP08056695-A. 05-MAR-1996. AAT28381; AA728381

AA7283

This is the nucleotide sequence of the human cytochrome P456 molecular species 259 gene which encodes a protein of 490 maino scide. The gene species 259 gene which encodes a protein of 490 maino scide. The gene wish when human liver derived cDNA library as 2 fragments of 0.9 and 0.6 kb using primers AAT2655.8. The prod. ass cloned into the 200 main and 0.6 kb using primers AAT2655.8. The prod. ass cloned into the 200 main and 0.6 kb using primers AAT2655.8. The prod. ass cloned into the 200 main and 0.6 kb using primers AAT2655.8. The prod. ass cloned into the 200 main and 200 main a or not rendered carcinogenic or "unsafe" if it is not d metabolised to a carcinogenic cpd. Sequence 1473 BP: 413 A: 345 C: 319 G: 396 T: 0 other:

and the state of the second of the state of the second of

Ouery Match 58.9%; Score 190.4; DB 17; Length 1473; Best Local Similarity 99.5%; Pred. No. 2.2e-5; Onservative Watches 13; Observative 0; Mismatches 1; Indels 0; Gaps

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The P-450 produced from plasmid phPA6 in a yeast expression system preferably Socriansonyces AM12, can be used for treat human liver disorders, oxidising various chemical substances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant plasmid, for yeast for liver treatment - comprises human liver cytochrome P-450MP gene obtd. from yeast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-450; cytochrome; Saccharomyces cerevisiae;
liver disorders; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruman liver cytochrome P-450 encoding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure: Fig 4; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ03599 standard; DNA; 1818 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AGEN ) AGENCY OF IND SCI TECH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-1988; 88JP-0225955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-1988; 88JP-0225955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1990 (first entry)
                                                                                                                                                                                                                                                                                                           WPI; 1990-121045/16.
P-PSDB; AAR04043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP02072879-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ03599;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AMO015599

      Q
                                                                                         Buman derived cytochrome; P450209; commercial cDNA library; yeast; transfection; recombinant production; expression vector; mammal; immuniation; densitiation; antibody; determination; detection; non-cross reactive; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes the human derived cytochrome (HDC) 945029, which was obted from a commercial cDNA library. Teast were transfected with an expression vector contg, the HDC cDNA cultured and then disrupted to give a nicrosomal fraction. The EDC was purified from the fraction, and used to lammalise and sensities a mammal. Blood vas drawn from the mammal, and an anti-HDC atthody isolated. The antibody obtd. recognises HDC 9405029, partic. at a serum dilution rate of 1:10000, and is substantially without cross reaction to other HDC 9450 spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody recognising human derived cytochrome P4502C9 - allows specific detection of cytochrome P450 species in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1473 BP; 413 A; 345 C; 319 G; 396 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Pages 11-13; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Busan derived cytochrome P4502C9 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT17404 standard; cDNA; 1473 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUME) SUMITONO CHEM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUL-1994; 94JP-0161551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-1994; 94JP-0161551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                   1139 tcattcccaagg 1150
                                                                                                                                                                                                                                                                                                    247 teatteecaagg 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-136337/14.
P-PSDB; AAR81465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP08027196-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boso saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAM-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT17404;
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Location/Qualifiers 1..1443 /*tag= a

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127 aagacaggagccacatgcctacacagatgctgtgtgtgcacgaggtccagagataccttg 186
                                                                        1; Indels 0; Gaps
                                              Score 190.4; DB 11; Length 1818; Best Local Similarity 99:54; Pred No. 2.4e-51; Hode Ratches 191; Conservative 0; Mismatches 1; Indels 0;
Sequence 1818 BP; 516 A; 412 C; 376 G; 514 T; 0 other;
                                                                                                          9.
9.
9.
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Overy Match 58-91; Score 190-4; DB 17; Length 1473; Bast Local Similarity 99:51; Pred No. 2.2e-51; Indels 0; Matches 191; Conservative 0; Mismatches 191; Indels 0;

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1029 aagacaggagccacatgccctacacagatgctgtggtgcacgaggtccagagatacattg 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytochrome P450 2C19; human; liver; PCR; primer; detection; CYP2C19; stereospecific 5-mephenytoin 4'-hydrox#lase activity; polymorphism; &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=-a
/product= Cytochrome P450 C9 clone 25
misc_difference 1085
                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome P450 2C9 clone 65 coding sequence.
                                                                                                                                                                                                                            RESULT 11
AAT11381
ID AAT11381 standard; CDNA; 1852 BP.
XX
                                                                                                                                                                                                                                                                                                                                                09-SEP-1996 (first entry)
                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09530766-A1.
                                                                                                                                                                                                                                                                                                           AAT11381;
        8 6 8 6 8
                                                                                                                                                                                                                                                                                                                The present invention describes a fusion proteins comprising a portion of a bacterial cyrochrome P400 protein and also a portion of a mammalian cyrochrome P400 protein and also a portion of a mammalian cyrochrome P400 protein. The fusion protein can oxidise hydrocarbons or any compound having a carbon-hydrogen boad. The fusion protein can be used for hydroxylating a compound to be oxidised. It can also be used in the bloremediation of an environmental pollutent. Since the fusion protein is anoluble, it can be subject to structural elucidation by X-ray expressed in soil becteria to facilitate bioremediation. The present sequence encodes amamalian cytochrome P450 protein CTP2C9 from the present invention.
                                Amgacaggagccacatgccctacacagatgctgtggtgcacgaggtccagagatacattg 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New P450 fusion proteins - comprising a portion of a bacterial cytochrome P450 protein and a portion of a mammalian cytochrome P450 protein
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacterial; mammalian; cytochrome P450; chimeric; fusion protein; oxidise; hydrocarbon; carbon hydrogen boad; hydroxylating; barromediation; environmental pollutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1845 BP; 507 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 Manmalian cytochrome P450 protein CYP2C9 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 10-11; 51pp; English.
                                                                                                                                                                                                                                                             AAX19925 standard; DNA; 1845 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1998; 98WO-US16979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AGG-1997; 97US-0056754
                                                                                                                                                                                                                                                                                                                                           11-JUM-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYRP ) UMIV ROCHESTER.
                                                                                                                 Jones JP, Shimoji M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-190131/16.
P-PSDB; AAX04127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HO9908812-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-PEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manmalla.
                                                                                                                                                                                                                                                                                                  AAX19925;
                                                                                                                                                                                                                    AXX19935

10 AXX19935

10 AXX19935

11 AXX19937

12 AXX1993

13 AXX1993

14 Bacteri

15 Bacteri

16 Bacteri

17 Ba
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/*tag= b /note= "Variable position" /*tag- c /note- "Variable position"

Location/Qualifiers 11..1483

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The sequences given in AAT11378-81 encode allelic variants of cytochrome 7450 C9. The majority of clones isolated from liver 533 coded for 259. The majority of clones isolated for 269. The 509 clones encoding 269, only two allelic variants were found. 39 of the 209 clones were identical with clone 55, and il were ledentical 39 of the 209 clones were identical with clone 55, and il were ledentical 39 of 31-noncoding regions but contained 2 single base changes at positions 50 of 01075 and 1435. One of these base changes was conservative but the other results in one amino acid difference at position 359. Ille to Leu. The clones 20c and 60 differ by one nuclectide in the coding region of the position 354. Anchor results in a single amino acid change. This to Met at position 355. Clone 25c has a very long, 198 bp. 5° noncoding region 50 has an unusually long 3' noncoding region containing three positiole 50 has an unusually long 3' noncoding region containing three positiole 50 has an unusually long 3' noncoding region containing three positiole 50 has an unusually long 3' noncoding region containing three positiole 50 non-coding regions could represent alternate splicing, allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated cytochrone P450 2c subfamily member - used for identifying drugs metabolised by 5-mephenytoin 4'-hydroxylase activity and to develop other screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                     De Morais SMF, Goldstein JA, Romkes-Sparks M;
                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 104; 169pp; English.
                                                                                          08-MAY-1995; 95WO-US05744.
                                                                                                                                                                                                          06-MAY-1994; 94US-0238821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-077257/08.
P-PSDB; AAR89865.
16-NOV-1995.
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Ouery Match 58.9%; Score 190.4; DB 20; Length 1845; Best Local Similarity 99.5%; Pred. No. 2.4e-51; Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps

127 asgacajagccacatgccctacacagatgctgtggtgcacagagtccagagataccttg 186

endobiotics such as steroids, fatty acids and prostaglandins.

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cc variants, or possibly separate genes. These clones are designated as callelly variants of ZGB because they differ by only one base in the coding region. They are most similar to ZG9 (82% maino acid homology).

XX and ZC19 (81% maino acid homology).

XX sequence 1852 BP: 514 A; 424 C; 380 G; 534 T; 0 other;
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187 acctectococcagoctgcccatgcagtgacctgtgacattaaattcagaaactatc 246 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 
Overy Match 58.94; Score 190.4; DB 17; Length 1852;
Best Local Similarity 99.54; Pred. No. 2.4e-51;
Matches ;191; Conservative 0; Hismatches 1; Indels 0; Gaps
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Human cytochrome P450 2C9 clone 65 cDNA AAV44157 standard; cDNA; 1852 BP 06-0CT-1998 (first entry) AAV44157; MANAMAN MANAMA

Cytochrome P450; drug screening; S-mephenytoin 4'-hydroxylase; identification; mutapenic; carcinogenic; cytotoxic; haemoprotein; xemobiotic; environmental poliutant; ss.

Homo sapiens. US5786191-A.

22-FEB-1994; 94US-0201118. 28-JUL-1998.

22-PEB-1994; 94US-0201118. 09-APR-1992; 92US-0864962.

(GOLD/) GOLDSTEIN J A. (ROMC/) ROMCES-SPARKS M.

Goldstein JA, Romkes-sparks M;

WPI; 1998-436528/37.

Screening for drugs metabolised by cytochrome P450 - for identifying mutagenic, carcinogenic, or cytotoxic compounds

Example 2; Column 53-56; 63pp; English.

This sequence encodes a human cytochrome P450 2C9 polypeptide isolated from clone 65. This polypeptide is used in a method to screen for a drug that is metholised by a cytochrome P450 having S-mephenytoin 4'-hydroxylase extivity. The protein can also be used to identify a mategaenic, cycloneme P450 are a large family of hemosprotein enzymes capable of metabolising xenoblotics such as drugs carcinogens and environmental pollutants as well as

Sequences AM51110-AM151593 represent human DNA fragments which contain bala leit te markers. The sequences are related to various human genes including microscanal glutathione 5-transferase II (MG5711), malate decarboxylase enzyme (DME1/ME1), cytcchrome P450, glutathione. Teductase/synthase (GME1/ME15), flavin-containing monocysquenses (FMO), gamma-glutamyltransferase 5 (GMF5), dipeptidase (DP), glucose 6-phosphate

Amyltrans.

Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping

Claim 13; Page 283; 673pp; English.

Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A;

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Ruman; biallelic marker; single nuclectide polymorphism: SNP; MGSTII; maircedecaboxylase enzyme; microsonal glutchinoe S-transferase II; malte decaboxylase enzyme; DMEI; cytochtorme P450; glutchinoe reductase; GSHR; GSHS; GGT9; If lavin-containing monoxygenase: PMO; gamm=glutchayltransferase 5; dipeptidase; DP; glutcose 6-phosphate dehydrogenase; G6PDH; haplotype; phosphoglucomate dehydrogenase; G6PDH; haplotype; uridine diphosphate glucoronosyl transferase; UGT2; asthma; hepatoxicity; illeuton; ds.
                                                                                                                                                                                                                                                                        Query Match 58.91; Score 190.4; DB 19; Length 1852;
Best Local Similarity 99.51; Pred. No. 2.4e-51;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruman CYP2CB related DNA containing a biallelic polymorphism SEQ ID
                                                            Sequence 1852 BP; 514 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
AAH51162.

AAH51162.

AAH51162.

AAH51162.

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debydrogenase (G6DDB), phosphogluconate dehydrogenase (PGDB), and uridine diphosphate glucoronosyl transferases (UGT2). Each of these sequences contains a biallelic marker/polymorphism, which is represented in the sequence as a degenerate/undefined base. The genes to which the bialloic marker containing sequences are related are involved in drug metabolism. Sequences AMB1518 represent the generate of the SETI game products PCR primers AMB15189 and AMB1509 and AMB1500 are MESTII game products PCR primers AMB15199 and AMB1500 are used in a cample for the amplification of human genomic DNA fragments. The invention includes a method of genotyping comprising determining the invention and unletted at a DNE or MCSTII related biallelic marker in a biological sample. The method is used to determine the frequency in compulation of an allele of a DNE or MCSTII related biallelic marker and to select an individual for inclusion in a clinical trial of a drug createment. The method is also used to detect association between haplotype and phenotype.

Createment and to detect association assays, sequencing assays or allele specific amplification assays. The method can association assays, sequencing assays assimate an individual saffers or is at risk of developing matters.
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Purifying recombinant cytochrome P450 · by utilising novel combinations of detergents and enzyme inhibitors

Disclosure; Column 55-56; 91pp; English.

Gillam EMJ, Guengerich FP, Guo Z, Sandhu

(UYVA-) UNIV VANDERBILT.

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Cytochrome P450; detergent; enzyme inhibitor; non-ionic; ionic; purification; drug oxidation; steroid; carcinogen; pesticide; human; ss.
                                                                                                                              Ouery Match 58.5%: Score 189; DB 21; Length 1001;
Best Local Similarity 93.3%; Pred. No. 5.1e-51;
Matches 251; Conservative 0; Mismatches 9; Indels 9; Gaps
                                                                                                                                                  Sequence 1001 BP; 251 A; 180 C; 193 G; 366 T; 11 other;
                                                                                                                                                                                                                                      Human cytochrome P450 2C10 variant DNA
                                                                                                                                                                                                                                                                            AAI22716 standard; DNA; 1419 BP.
                                                                                                                                                                                                                                                                                                                                                                    9405-0194981.
                                                                                                                                                                                                                                                                                                                                                                            10-FEB-1994; 94US-0194981.
                                                                                                                                                                                                                                                                                              27-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                    10-FEB-1994;
                                                                                                                                                                                                                                                                                                                                              US5436157-A.
                                                                                                                                                                                                                                                                                                                                                         23-MAR-1999.
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This invention describes a recombinant cytochrome P450 protein which is purified from a host cell culture using a combination of detergents and enzyme inhibitors. The method comprises (a) fractionating the host cells to prepare their membranes, (b) adding a non-ionic detergent to the membranes, (b) adding a non-ionic detergent to the membranes in a concentration of 0.8 % to 2% % tw/v) in a detergent to the membranes in a concentration of 0.8 % to 2% with a non-ionic detergent to the membranes in a concentration of 0.4% to 0.8% w/v) in a detergent to the membranes in a concentration of 0.4% to 0.8% w/v) in a purifying the protein ratio of between 2:1 to 4:1 (d) centrifuging the protein through a diethylaminoethyl-beaded column, then through a carboxymethyl-beaded column, and finally through a carboxymethyl-beaded column, and finally through a carboxymethyl-beaded column, and finally through a carboxymethyle or catalysing the oxidation of drugs, steroids, carcinogens and pesticides. The method simplifies the column for M450 proteins by the use of improved expression vectors and novel detergent combinations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome P450; detergent; enzyme inhibitor; non-ionic; ionic; purification; drug oxidation; steroid; carcinogen; pesticide; human; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 58.51: Sorore 188 B. DB 20; Length 1419; Best Local Similarity 99.01; Pred. No. 6.9e-51; Indels O: Gaps Matches 190; Conservative O: Mismatches 2; Indels O: Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1419 BP; 409 A; 332 C; 307 G; 371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytochrome P450 2C10 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX22715 standard; DNA; 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-1999.
10-FEB-1994; 94US-0194981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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10-FEB-1994; 94US-0194981
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(UTVA-) UNIV VANDERBILT.

Gillam EMJ, Guengerich FP, Guo Z, Sandhu P;

WPI; 1999-228609/19.

Purifying recombinant cytochrome P450 · by utilising novel combinations of detergents and enzyme inhibitors

This invention describes a recombinant cytochrome P450 protein which is purified from a host cell culture using a combination of detergents and engrge inhibitors. The method comprises (a) fractionating the host cells to prepare their membranes, (b) adding a non-ionic detergent to the membranes (b) adding a non-ionic detergent to the membranes in a concentration of 0.8% to 2% tells in a tell of between 4:1 to 10:1, (c) adding an ionic detergent to the membranes in a concentration of 0.4% to 0.8% v/v) in a cetergent protein ratio of between 4:1 to 10:1, (c) adding an ionic detergent protein ratio of between 2:1 to 4:1 (d) centrifuging the membrane-detergent mixture to remore insoluble materials and (e) purify trying the protein through a deterhyminoschyl-beaded column, then chrough a carboxymethyl-beaded column, and finally through an ordering super to purify cycochrome P450 corteins which are responsible for catalysing the oxidation of e150 corteins which are responsible for catalysing the oxidation of e160 purify cycochrome P450 proteins and pesticides. The method simplifies the complement of P450 proteins, by the use of improved expression vectors and novel detergent combinations. Disclosure; Column 53-54; 91pp; English.

Sequence 1591 BP; 443 A; 372 C; 353 G; 423 T; 0 other;

67 cagctaaagtccaggaagagattgaacgtgtgattggcagaaaccggagcccctgcatgc 126
959 cagctaaagtccaggaagagattgaacgtgtgattggcagaaaccggagccctgcatgc 1018 Ouery Match 59.5%; Score 188.8; DB 20; Length 1591; Best Local Similarity 99.0%; Pred No. 73e-51; Matches 19; Conservative O; Mismatches 2; Indels 0; Canada Š

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Search completed: April 19, 2002, 08:15:33 Job time: 3233 sec

188.8 58.5 802 11 BG217233 188.8 58.5 876 11 BG196822	188.8 58.5 896 11 BG197837 188.8 58.5 910 11 BG19848 187.4 58.0 791 11 BG198890 187.2 58.0 893 11 BG195327	Seconds 19 187.2 58.0 899 11 BG202484 BG202484 BC202484 BC202484 BC202484 BC202484 BC202484 BC202484 BC202484 BC202484 BC202484 BC2025956 BC241656 BC241666 BC241666 BC241666 BC241666 BC241666 BC241666	23 183.5 57.2 864 11 86203446 25 180.8 56.0 595 10 AV658393 26 179.2 85.5 402 10 AV658335 27 175.4 64.3 76.0 10 AV652375	170.4 53.1 928 11 BG20597 170.8 52.9 619 10 AV550106 165 51 619 11 BG1088	165.4 51.5 513 11 EXTENSION 1165.1 158.6 49.1 525 10 AI314364	C 33 158.6 49.1 577 10 AA106162 34 158.6 49.1 779 10 AA822587	158.6 49.1 821 10 A1047293 158.6 49.1 833 10 A1097741 157 48.6 535 10 A570947	157. 48.6 578 11 BF660352 155.6 48.2 778 10 A1116382 153.6 47.6 350 10 AV681651 153.6 47.6 355 10 AV655278	153.6 47.6 377 152.6 47.2 378 151.8 47.0 614 150.4 46.6 356	ALIGNMENTS	AV658443 599 bp mRNA EST	DEFINITION AV658443 GLC Homo sapiens cDNA clone GLCFWE09 3', mRNA sequence ACCESSION AV658443 VERSION AV658443.1 GI:9879457 KEYNORDS EST.	SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENC AUTHOR	TITLE	CONNENT Contact: Zeguang Han Cenome Center at Shanghai		AV658443 AV65843 Fax: 86-21-50801922 AV658435 AV656435 This clone is available at CHCC in Shanghai. FRATURES Location/Oualifiers	nos		51261 AV651261 /dev_stage="Adult" /dev_stage="Adult
n 4.5	Copyright (c) 1993 · 2000 Compugen Ltd.	April 19, 2002, 08:07:49; Search time 2723.34 Seconds (without alignments) 1274.496 Million cell updates/sec	US-09-763-292-3 323 1 ccctgaattgctacaacaaaaattcatagtatcatttt 333	IDENTITE_NUC Gapop 10.0 , Gapert 1.0	11351937 seqs, 5372889281 residues	Total number of hits satisfying chosen parameters: 22703874	Minisum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries				gb_htc:* gb_gss:* em_gss_fun:* em_gss_hun:*	em_gss_hn:* em_gss_ph:* em_gss_pro:*	em_gss_vrt:* em_gss_other:*	*Pred. **Do. 1s the number of results predicted by chance to have a soore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMARIES	Query Match Length DB ID Desc	AV658435 AV658435 AV646130 BC215664	BG567504 BG186520	BG205398 BG205076 BG19889 BG184407	AV651261 AV652420

BASE COUNT ORIGIN

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Notefild 614 bp mRNA EST 07-SEP-2000

Notefild GLC Homo saplens CDNA clone GLCAJG07 3', mRNA sequence.

Notefild GLC Homo saplens CDNA clone GLCAJG07 3', mRNA sequence.

Notefild GLC Homo saplens CDNA clone GLCAJG07 3', mRNA sequence.

SET. 10 1:9867144

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/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
host
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Best Local Similarity 99.54; Pred. No. 5e-41;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps
Oy 67 cagetaaagtccaggaagagttgaacgtgtgattggcagaaaccggagcccctgcatgc 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 58.9%; Score 190.4; DB 10; Length 599; Best Local Similarity 99.5%; Pred. No. 55-41; Indels 0; Gaps Matches 191; Conservative 0; Mismatches 11; Indels 0; Gaps
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1. Gillon, Controlled State of the Control of the Control of Controlled State of Contr
                                                                                                                               BG186520 856 bp mRNA EST 21-APR-2001
RST5587 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
BG186520.1 GI:13708207
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Best Local Similarity 99.5%: Pred. No. 5.1e-41;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps
nRNA sequence.
BG567504
BG567504.1 GI:13575157
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Rome sapiens

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Rolayfork; Metazoa: Chordata; Craniata; Vertebrata; Euteleostcomi:

Rolayform, J., Sheff, B., Rundlett, S., Jackson, P. D., Perry, R.,

Cain, S., Dahl, T., Thornton, M. Ramachandran, R., Whittigopton, J.,

Idener, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E.,

Valoso, M., Ress, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.,

and Dozar, M. Ress, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.,

and Dozar, M. Ress, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.,

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Andersys, Inc.

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DEFINITION 601986139F1 NIH_MGC_76 Homo sapiens CDNA clone INACE:4715312 5:
                                                                                                                                                                                                                                                                                           BG215664 779 bp mRNA EST 21-APR-2001
BG215313 Athersys RACE Library Homo sapiens cDNA, mRNA sequence.
BG215664.1 G1:13741685
BG215664.1 G1:13741685
human.
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287 TCATTCCCAAGG 298
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BG205076 BG205076 I GI:13726763 ESG Library Homo sapiens CDNA, mRNA sequence.
BG205076.1 GI:13726763 ESG.
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High quality sequence stop: 433.

Location/Qualifiers

1. 901

Angerial Parkon: 9606

/ Aref - taxon: 9606

/ Cell_line="Hil080"

/ Notes="See 'Creation of Genome-wide Protein Expr

Innee="See 'Creation of Genome-wide Protein Expr

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cell type indicated is Hil080, since a random ac

method was used, these sequence tags are not nec

expressed in Hil080 under normal circumstances.

T 230 a 241 c 199 9 231 t.
                        Nat. Biotechnol. 19 (5), 440 (2001) In press Contact: Scott J. Cain
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3101 Carnegle Are, Cleveland, OH 44115,
Tel: 216 431 9900
Fax: 216 384 5956
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110 cactanagtccaggaagaattgaacgtggattgcagcaaaacggagcccgcatgc 126
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Explaints. Heleacas: Chordata; Craniata; Vertebrata; Enteleostomi; Medrayota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Medrayota; Lutheria; Primates; Catarfulii; Hominidae; Homeo.

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112 AAGACAGACCAATGCCTACACATGCTGTGTGTGAAGAGGTCGAGAATACATT 171
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Contact: Scott J. Cain
Activation of Gene Expression Libraries using Random Activation of Gene Expression (15 431 9958; Inc.
3701 Carnegie Ave. Cleveland, OH 44115, USA
Tel: 216 431 9959
Fax: 216 431 9960
Fax: 216 431 9960
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Cell line-"H1000' of Genewa-wide Protein Expression Libraries using Random Activation of Genewa-wide Protein Expression'
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E Harrington.J.J.; Sheff.B.; Rundlett.S., Jackson.P.D.; Perry.R.; Cain.S., Dahl.T. Thorncon.M.; Ramachandran.R.; Mhittington.J.; Veloso.N.; Hass.J.; Cothren.K., Clerk.S.; Mays.R.; Smith.E.; Veloso.N.; Hass.J.; Cothren.K.; Offenbacher.J.; Danzig.J.; and Ducar.M.
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Raberrycka: Metacoa: Chordata: Craniata: Vertebrata: Euteleostomi: Memalia.

Ramania: Eurbharia Frimates: Catarrhini; Hominidae; Homo.

Acains: Dabl. 7. Sherf. B., Rundlett. S. Jackson, P. D., Perry R., Cains. J., Sherf. B., Rundlett. S., Jackson, P. D., Perry R., Raringoton, J. J., Sherf. B., Rundlett. S., Jackson, P. D., Perry R., Sherf. B., Resiligott. R., Clark S., Whitington, J., Lanes, J., Cohneun. K., Lor. R., Offenbacher, J., Marshoc, D., Merziligott. R., Ciark S., Ways. R., Smith. E., Canton of Gene Expression

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BG217233 802 bp mRNA EST 21-APR-2001
82756935 Athersys RACE Library Homo sapiens cDNA, mRNA sequence.
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Owery Match 58.51; Score 188.8; DB 11; Length 896; Best Local Similarity 99.0%, Pred No 1.4e-40; Indels 9; Matches 199; Conservative 0; Mismatches 2; Indels 0; Gaps
Contact: Scott J. Cain
Athersys. Inc.
3101 Carnegle Ave. Cleveland, OH 44115, USA
Far: 216 361 9596
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High quality sequence stop: 321.
Location/Qualitiers
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Search completed: April 19, 2002, 08:07:52 Job time: 2772 sec

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19.4%: Score 62.8; DB 6; Length 591;
Best Local Similarity 58.3%; Pred. No. 3.1e-10;
Matches 109; Conservative 0; Mismatches 78; Indels
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US-10-105 299-13254
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US-10-106-698-858
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NNISH: Homo sapiens
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7. cqq12_6/ptodata/J/pna/PCT_NEW_CONB.seq:*

7. cqq12_6/ptodata/J/pna/NS06_NEW_CONB.seq:*

7. cqq12_6/ptodata/J/pna/NS08_NEW_CONB.seq:*

7. cqq12_6/ptodata/J/pna/NS08_NEW_CONB.seq:*

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7. cqq12_6/ptodata/J/pna/NS08_NEW_CONB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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US-10-103-313-621
US-10-103-313-621
Sequence 621, Application US/10103313
Sequence 621, Application US/10103313
SEQUENCE 621
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJ07C11
CURRENT FILM GAME: 2002-03-12
CURRENT FILM GAME: 2002-03-12
NUMBER 0 SDQ 1D MOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTAME: Patentin Ver. 2.0
SDQ 1D MO 621
LENGIH: 1186
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Matches 85; Conservative 0; Mismatches 50; Indels 'Mismatches 85; Conservative 18.00 Mismatches 18.00 Mismatches 18.00 Mismatches 18.00 Mismatches 19.00 Mismatc
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LOCATION: (518)
OTHER INFORMATION: n equals a,t,9, or c
NAME/KET misc_teature
LOCATION: (921). (523)
OTHER INFORMATION: n equals a,t,9, or c
US-10-106-698-2440
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ORGANISH: Homo sapiens
US-10-103-313-621
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US-10-105-299-7204/c
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ITILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and PolyFertidd
FILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and PolyFertidd
FILE REFERENCE: PAGOS 1

CUBRETA APPLICATION NUMBER: US/10/106,698

CUBRETA APPLICATION NUMBER: PCT/US00/26524

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR PILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR FILING DATE: 1999-11-03

PRIOR FILING DATE: 2000-11-03

PRIOR FILING 
67 gctcacatgccctacaccactgccgtgattcatgaggtgcagcgctttggggacatcgtc 126
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LCCATION: (461). (462)'
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KET: misc_feature
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ORGANISM: Homo saplens
FEATURE:
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LOCATION: (4)..(4)
OTHER INFORMATION: n eq
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187 aagggaa 193
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bb 9331 GAAGAACCGTGAACCTGAAGCCCGCCCCCAACCTGACTATGCGTGTG 9392
CAAGAACCAACCCTGTAAGACCTGAAGCCCGCCCCCCCAACCTGAACTATGCGTGTG 9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9231 GGGCTGCGGGGACCCTCGACGCCACCTGCACACCCACTGTCTGCCCCAAAGGT 9172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Watch

13.81: Score 44.6; DB 6: Length 1186:
Best Local Similarity 53.14; Pred. No. 0.00014:
Matches 95; Conservative 0: Hismatches 84; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
12.0%: Score 18.6; DB 6; Length 13327:
Best Local Similarity 50.8%; Pred Wo. 0.028;
Watches 9; Conservative 0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5

US-10-105-299-7201/C

Sequence 7201, Application US/10105299

GENERAL IMPORATION:
GENERAL IMPORATION:
HILL OF INVESTION:
FILE REPRESECT: PSSS Guman Secreted Proteins
FILE REPRESECT: PSSS Guman Secreted Proteins
FURREST APPLICATION NOMER: US/10/105, 299

CURREST APPLIATION NOMER: 2002-03-26

NUMBER OF SED ID NOS: 15197

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

LEASTH: 13377
                                                                     or Palm
CORRER OF TOTACE DATE: 2007-03-26

NUMBER OF SEQ 1D MOS: 15197

PRIOR APPLICATION TEROVED. See Fille Wrapper (*)

SECTION APPLICATION TEROVED. 3

SECTION NO 7204

LEMENTE: DAM.

TERE: DAM.

OCAMAISH: SECTION SEE SECTION SEE SECTION SEED SECTION SECTION
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; ORGANISM: Homo sapiens
US-10-105-299-7201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 a 260
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200 cagcctgccccatgcagtgacctgtgacattaaattcagaaactatctcattcccaaggt 259
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                                                                                                                                                                                                                                                                                                                                                                                                       11.5%; Score 37; DB 6; Length 1182; 50.3%; Pred. No. 0.03; tive 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                           Query Watch 1154: Score 37: DB 6: Length 1182: Best Local Similarity 50.3%; Pred: NO 0.03; On 10.09 Watches 91; Conservative 0: Wismatches 99; Indels
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJZ07C1
     CURRENT APPLICATION NUMBER: US/10/103.313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SED ID NOS: 653
FILING APPLICATION FERONAGE - See File Wrapper or Palm: SOFTAME: Patentin Ver. 2.0
LENTIL 182
LENTIL 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 105-239-7203/C
US-10-105-239-7203/C
Sequence 7203. Application US/10105299
Sequence 7203. Application US/10105299
GENERAL INFORMATION:
TITLE CE INVENTION: Human Secreted Proteins
TILLE OF INVENTION: Human Secreted Proteins
CURRENT FAPLICATION NUMBER: US/10/105.299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID MOS: 1910-03-26
NUMBER OF SEQ ID MOS: 1910-03-26
SOFTHARE: PARENLIN VET. 2.0
SOFTHARE: LENGTH: 1802
LENGTH: 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 50.30
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-7203
                                                                                                                                                                        TYPE: DNA
GORGANISM: Homo sapiens
US-10-103-313-622
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4220 CIGAAGGCAGCTICAGAGCCACTIGCCAGGCTGAGAACTATCCGGGCTCAGTGCTCTCT 4161
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                                                                                                                                                                                           199 ccagcctgccccatgcagtgacctgtgacattaaattcagaaactatctcattccca 255
                                                                                                                                                                                                                                                                                                66 tigigetaacacatgetgigaetgageccaccactitgggagggtatgacataccaa 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
9.31: Score 30.2; DB 6: Length 35959;
Best Local Similarity 52.84: Pred. No. 15;
Best Conservative 0: Mismatches 58: Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 9.1%; Score 20.4; DB 6: Length 589; Best Local Similarity 56.8%; Pred: No. 4.5; Wardhes 54; Conservative 0; Wismatches 41; Indels (Matches 54); Conservative 10; Wismatches 54; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-ESULT 10.105-299-10167/c

1S-EQUENCE 10167, Application US/10105299

1S-EQUENCE 10167, Application US/10105299

1S-EQUENCE INFORMATION:

1TILE OF INVENTION Human Secreted Proteins

1TILE REFERENCE: PSS90

1CURRENT FILING DATE: 2002-03-26

1CURRENT FILING DATE: 2002-03-26

1NUMBER OF SEQ 10 MOS: 13197

1FIOT Application removed . See File Wrapper or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : NAME/KEY: misc_feature
: LOCATION: 440, 454, 480, 538, 559, 566, 587
: OTHER INFORMATION: n = A.I.C or G
US-10-015-219-101
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TITLE OF INVENTIONS: COMPOSITIONS AND DIAGNOSIS OF OVAR
FILE REPERACE: 21011.49301
CURRENT APLICATION WOMBER: 02/10/219
CURRENT FILLING DATE: 2002-03-02
NUMBER OF SEO ID NOS: 1739
SOFTAME: FasiSED for Windows Version 4.0
SOFTAME: FasiSED for Windows Version 4.0
LEMENT: 589
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SANISM: Homo sapiens
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                                                                                                                        APPLICATE NUMBER 18.

FITTE PREVENCE: PRODUCT
FILE PREVENCE: 2000-09-28-27
FILE PREVENCE: 2000-09-28
FILE PREVENCE: PRODUCT
FILE PREVENCE: 2000-09-28
FILE PREVENCE: 2000-09-29
FILE PREVENCE: 2000-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Owery Match 9.51; Score 30.6; DB 5; Length 254; Best Local Similarity 53.84; Pred. No. 1.3; Observative 9; Marches 63; Conservative 0; Mismatches 54; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700955037H1
US-09-975-254-18019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COTHER INFORMATION: n equals a,t,g, or c US-10-106-698-892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equals a, t, g, or c
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Sequence 18019, Application US/09975254
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIPE: DNA
ORGANISM: Bomo sapiens
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Db 234 CTCCATANTTOTACATTATCATTGCCAGGGTTCTCCTCGCTCAGCTTTTGCTGGTA 175

Oy 61 tcttatcagctaaagtccaggaagattgaagqt 95

Oy 61 tcttatcagctaaagtccaggaagattgaagqt 95

D 174 TTTCTTCTGCAGCTCCTCAAGTTGAGTCTGCAGGT 140

RESGLT 12

US-10105-299-2978

N-PPLICANT: Rosen, et. al.

TITLE OF INTERTION: Human Secreted Proteins

FILE REPRENCE: 89950

COTREAT FILLING DATE: 2002-1256

NUMBER OF 892 ID NAS: 15137

PLOT APPLICATION NUMBER: US-107-16

SOUTHARE PRENCE: 89950

COTREAT PLILING DATE: 2002-1256

NUMBER OF 892 ID NAS: 15137

PLOT APPLICATION TSONOG- See File Wrapper or Palm

SEQUENCE: Date: 103

SEQUENCE: 103

SOUTHARE PRENCE: 103

LENGTR: 103

LENGTR: 103
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RESULT 13
US-10-105-299-14978
Sequence 1407b Application US/10105299
Sequence 1407b Application US/10105299
SEREMAL INFORMATION:
APPLICANT: ROSEN, et a.
ITILE OF INVENTION: Human Secreted Proteins
FILE PREFERENT: PS950
CURRENT APPLICATION WIMBER: US/10/105,299
CURRENT PILICATION NUMBER: US/10/105,299
WIMBER OF SDD IN SC: 15197
PFLOT APPLICATION FEMOVED: See File Wrapper or Palm SDD IN 80 14978
LEMORER # PATENTION FEMOVED: A CONTRAINER PATENTI

Ouery Match 9.11; Score 29.4; DB 6; Length 4587;
Best Local Similarity 50.3N; Pred. No. 11;
Matches 72; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Cy 155 tgctgggtgcagagatggtagaactggaagcaaggcagctaccttttgcanaaggaaa 4176
Cy 155 tgctgggtgcacgagqtccaga 177
Db 4177 tggtgttagqcacgagtccaga 177
Db 4177 tggtgttagqcccttttccaga 179
PESULT 14
PCT-USO2-07787-34/C
GENERAL INFORMATION:
APPLICANT: The Brigham and Women: S Hospital, Inc.
APPLICANT: SWINGER: SOUTH S HOSPITAL SWINGER: SOUTH S HOSPITAL SWINGER: SOUTH S HOSPITAL SWINGER: SAUTH S HOSPITAL SWINGER: SW
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Very Vactor actual type 22.74: Fred. 62.44: DB 9; Length 140.10;
Best Local Similarity 52.74: Fred. No. 18;
Matches 63: Conservative 0: Mismatches 56: Indels 0: Gaps 0:
Cy 75 gtccaggaagattgaacgigtgattgacagaaaccggagcccctgcatgcaagacagg 134
Db 6435 GACCTGGAGAGCACCCCGGTGGAGTGGAGTGCCTTGAGCAAAGGG 6376

Mon Apr 22 08:41:41 2002

Description

	GenCore version 4.5	Result No.	Score	Query Match Length	ength D	DB 1D	0	
		1	1739.6	99.6	1746	9 B	AR071575 HIMCYPC219	
OM nurleic - nuc	- nucleic search, using sw model	1 m =	1632.4	93.5	1669	E LE To ov	E14931	
Run or.:	April 19, 2002, 07:21:40 ; Search time 4168.4 Seconds (without alignments) (without alignments) (910,103 Million cell updates/sec	* 80 0 1	1534.6 1529.8 1529.8	87.9 87.6 87.6	1852 1854 1854		AR071579 AR071576 HUMCYP2C9	
Title Perfert score: Sequence:	US-09-763-292-1 1746 1 cttcmatggatccttttgtgacmatattattattaaaaga 1746	8 9 10 11	1506.4 1501.8 1495.8 1458.6	86.3 85.7 83.7	1843 1826 1814 1473		E02279 HUMCYPH2 S46963 E10866	
Scoring table:	IDEMITIT_NUC Gapop 10:0 , Gapext 1.0	123	1456.4 1436.4 1413.6	83.4 81.0	2395 1892 1444	000 E 4 M	HUMSVP450A AR071581 E14930	
Searc!.ed:	1472140 seqs, 8248589755 residues	16	1366.6	78.3	1576	20 EE	HUMCY PMPA HUMCY PMP	
Total number of	Total number of hits satisfying chosen parameters: 2944280	181	1343.4	76.9	1473	77	E10853	
Minimum DB seq length: 0	length: 0 length: 2000000000	20 21 21	1264.6	77.77	2009	 	AR071577 AR071580	
Post-processing:	Post-processing: Minimum Match ON Maximum Match 100% Maximum Match 100% Listing Match 100% Listing first 45 summaries	52 53 53 53 55 55 55 55 55 55 55 55 55 55	1238.8	57.0 57.8 57.8	1346		HSCP450 HUMCYP2C17 HSIIC2	
Database :	GenEmbl: *	27	1173.8		1473	22 4	553045 E10865	
	1: 95-ba:* 2: 95-btg:* 3: 95-btg:*	29 29 30	1170		1829		HUMCY PAX HUMCY PAX	
	4: 9b_on:* 5: gb_ov:*	32	1138.6		1441		HUMCY PMPB HUMCY PB	
	6: 9b_pat:*	33	1109.8 1109.8	53.6 53.6	1473	22	E10639 E10862	
•	197-191.4 197-191.4 197-191.4	35	1106.6		1473	22	E10863	
		37.0	1097.8		1737	m 4	HUMCYPMPD	
	11: yu_sus: 12: gb_sy:*	99	1074.4		2340	· ~	ABCYP2C5	
	13: gb_un:* 14: gb_v1:*	7 7	1055 1061.2	51.0 50.8	1662	~ ~ ⊠ ⊠	RABP45HP3	
		42	1055.2	50.4	1871	K 4	RABCY 4501	
	16: em_tun:* 17: em_hum:*	7 7	1038.6	29.5	1758		SSC15D09	
		45	1038.2	59.5	1808	10	HAMP4502	
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								2
	23: em_ph:* 24: em_pl:*	RESULT	1					
		AR071575		21515	1746	ŝ	420	
	70: em_sts:" 27: em_sv:*	DEFINITION		uence 2	from pa	atent	Sequence 2 from patent US 5912120.	.0
		ACCESSION		171575	. ;			
		VERSION		AR071575.1	GI:/222463	22463		
		SOURCE		Unkno-n				
	32: em_htgo_rod:*	ORGANISM		Unknown.	7			
		BEFERENCE		(bases	to 17	46)		
	35: em_htg_rod:* 36: em_htg_other:*	AUTHORS TITLE		dstein,	J.A. and xpression	d De	Goldstein,J.A. and De Morais,S.M.F. Cloning, expression and diagnosis o	Is of
	a country of the state of the s	Telegion		princi	pal det	ermin	the principal determinant of s-mephe	nephe
score grea	Fred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,	FEATURES	ٔ د	, A -	Location/Qualifiers	/0.na	ifiers	;
and is der	lyed by analysis of the total score distribution.	D _S	source	- <	organis	ш. -ш.	known	

of human cytochrome P450 2C19: phenytoin metabolism

/organism="unknown" 477 a 418 c 365 g

BASE COUNT ORIGIN

18-FEB-2000

PAT

SUMMARIES

Page 2

09 1021 tycacgacagggccacatgccctacacagatgctgtggtgcacgaggtccagggataca 1080	1201 aagaatttcccaacccagagatqtttgacctcqtcacttctqqatgaaqttt	0y 1331 gectggccgcatgagctgttttattcctgaccttcatttacagaactttaactga 1380 1321 GCTGGCCCGCATGAGCTGTTTATTCCTGACTTTAACTGAACTTTAACTGA 1380 0y 1381 aatctctgatgccaaaggaccttgacacactcctgttgtcattggttctg 1440	1441 TCCCCCTTCTTTTTTTTTTTTTTTTTTTTTTTTTT		Oy 1741 adataga 1746 Db 1741 AATAGA 1746 RESULT 2 HUNCYPC219	LOCUS HUNCYPCAL) 1746 bp mRNA PRI 31-DEC-1994 DEFINITION HUMAN CYTOCHTOM P\$50219 (CYP2C19) mRNA, clone 11a. ACCESSION 961854 J053166 me P\$502019 (CYP2C19) mRNA, clone 11a. ACCESSION 961854 J053166 me P\$502019 (CYP2C19) KRIWADS CYTOCHTOM FOR THE CONTROL ORGANISM ENDA CYTOCHTOM FOR MANA. ORGANISM ENDA CYTOCHTOM FOR THE CAST CALACTAIN; Hominidae: Homo. REFERENCE TO TAKE TO TAKE TO TAKE THE CAST CALACTAIN; Hominidae: Homo. AUTHORS CONTROL ORGANISM ENDA CYTOCHTOM FOR THE CAST CAST CAST CAST CAST CAST CAST CAST
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    /organism-'Homo sapiens'
    /tissue_type-'liver'
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1 (bases 1 to 1852)
Coldstellu, J.A. and De Morais, S.M.F.
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Colosto, expression and diagnosis of human cytochrome P450 2019:
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ä Ouery Match 87.61; Score 1529.8; DB 6; Length 1854; Best Local Similarity 92.74; Pred. 70. 0; Matches 1544; Conservative 0; Mismatches 112; Indels 17; Gaps

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1 (bases 1 to 1854)

Rondes, M., Faletto, M.B., Blaisdell, J.A., Raucy, J.L. and
Rondes, M., Faletto, M.B., Blaisdell, J.A., Raucy, J.L. and
Cloning and expression of complementary DNAs for multiple members
of the human cytochrome P45011C subfamily (published erratum
appears in Blochemistry 1993 Feb 9:32(5):1390)
Blochemistry 30 (13), 3247-3255 (1991)
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Matches 1634; Conservative (
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Score 1529.8; DB 9; Length 1854; Pred. No. 0; 0; Mismatches 112; Indels 17; Gaps

Location/Qualifiers
//crganiam-Homo sapiens*
//crser-taxon:9606*
//drser-taxon:9606*
//drser-tracon-713:..1489
//drser-crp2c9*

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481 coasgettcacctgtgatcccatttcacctgggctgtgtccctgcaatgtatct 540 [IIIII | IIIIIII | IIIII | IIIII | IIII | IIIII | IIIII | IIIII | IIIII | IIII | IIIII | IIII | IIIII | IIII | IIIII | IIII | IIIII | IIII | IIIII | IIII | IIIII | IIII | IIIII | IIII | IIIII | IIII | IIIII | IIII | IIII | IIII | IIII | IIII | IIII | IIIII | IIIII | I
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HUNCTP2C9 1854 bp mRNA, PRI 31-DEC-1994 (MRNA clone 25. MRNA CNOTE MRNA CLONE 25. MRNA CNOTE MRNA CLONE PAGE 27. GCT-1813101 (MRNA CNOTE 27. GCT-1813101 (MRNA TYCL) MRCA CNOTE 27. MRNA TYCL) MRCA CNOTE 27. MRCA CNOTE 27. MRNA TYCL) MRCA CNOTE 27. MRCA TYCL) MRCA CNOTE 27. MRCA TYCL) MRCA TYC

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RESULT 7
HUMCYP2C9

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Page 9

E02279 LOCUS DEFINITION Human liver cytochrome P450MP gene. ACKESSION E02279 VERSION E02279 KEWORNS Homo sapiens: ONGANISM Homo sapiens ENATYOCA: Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi; Memmalia: Eutheria: Primates; Catarrhini: Homonidae: Homo.	AUTHORS OQIYO, JINTIKI,N., FUJILDAI,T., Kamatakl,T., Komori,M. and Miura,T. TIILE RECOMBINANT PLASMID INTEGRATED WITH GENE OF HUMAN LIVER CYTOCHROWE P. 400HP. FRAST PRODUCING P. 450HP. FAND JOURNAL PERENE: JP 1990072879-A 1 13-MAR-1990; COMMENT OF IND SCIENCE & TECHNOL COMMENT PH JP 1990072879-A/1	PD 13-MAR-1990 PD 13-MAR-1990 PD 105-MAR-1990 PT OGITA SATORU. JINRIKI NARIKO, FÜJITANI TOMOMICHI, PI KANATAKI TETSUYA, HUNBA TOSHIAKI PT KOMOMI MASAVUKI, MIURA TOSHIAKI PR CATAIS/53.(ZIAN/16.CIZNIS/81,(CIZNI/16,CIZRI:865); CC CT LOPOLOGY: Linear: CC topology: Linear: CC topology: Linear: CC anti-sense: No:	*source Key Key CDS	FEATURES 1.0ccation/Outliflers source /organism-*Homo saplens* (Ab_xref-*taxon:9606* BASE COUNT 512 a 424 c 377 g 530 t	Ouery Match Best Local Similarity 92.4%; Pred. No. 0; Best Local Similarity 92.4%; Pred. No. 0; Matches 1626; Conservative 0; Matches 1626; Conservative 0; Marmatches 1626; Conservative 0; A catggarcettrgtgetetgetetgetetetetetetetetetet 63 Filling	64 63 124	184 tetatggecetgtgtteactetgtattttggectggaacgeatggtggtgetgeatggat
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Mode" 21 a nucleotides" S04 a 421 c 377 g 524 t	oy.	976 aggaaggaattgaacgtgtcattggcagaaacggagccctgcatgca
Ouery Match 86.0%; Score 1501.8; DB 9; Length 1826; Best Local Similarity 92.5%; Pred. No. 0; Matches 1618; Conservative 0; Mismatches 112; Indels 19; Gaps 3;	ර් සි	1035 acatgccctacacagatgctgtgqtqcacgaggtccagagatacatcgacctcatcccca 1095
ttgtggccttgtgctctgtgctccatgtttgcttctcctttcaatctggggacagagct 75 	a où	1096 cragocidacceatgeagracipidaccipidacquaaaactaacccaatccaagg 1155
ctgggagagaaactcctcctggcccactcctctcccagtgattggaatatcctac 135 	B 33	
agatagatattaaggatgtcagcaaatccttaaccaatctctcaaaaatctatggcctg 195 	÷ 6	1216 cagagatgitigaccicgicaciticiggaigaaggiggaaatitlaagaaaagaaci 1275
<pre>tgttcactctgtattttggcctggaacgcatggtggtgctgcatggatatcgaactggtga 255 </pre>	සි හි	1276 acttcatgcctttctcagcaggaaaacggatttgtgtgggagagggctggcccgcatgg 1335
356 aggaagccctgattgatcttggagaggttttctggaagaggcatttcccactggctg 315	යි ර	1336 agretettitaticcigaccticatitiaacagaactitaactigaacicidatigace 1395
Ltttagcaatggaaagagatggaaggagttc 	<i>8</i> 8	1396 caaagacctigacacaactcctgitgicaatgaattgctctgtccgccttctatc 1455
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	S S	1626aaaaagtttcactgtgcaaatatatctgctattccccatactctataatagt 1677 IIIR
acatcaggattgtaagcacccctggatccagatatgcaataatttcccactatcattg 575 		tacattgagt GCATTGAC
<pre>attatttcccgggaacccataacaaattacttaacaaccttgctttatqgaaagtgata 735 III </pre>	Oy Dp	1738 ttaataga 1746
tttiggagaagtaaagaacaccaagaatcgatggacatcaacaaccctcgggacttta 795 	RESULT 10 S45963 LOCUS	
tgattgcttcctgatcaaatggagaaggaaagcaaaccaacatccgaatccacta 855 	ACCESSION VERSION REYWORDS	putative CYPC2C9 gene human. liver. mRNA. 1814 546963
ttgaaaacttggtaatcactgcagctgacttacttggagctggactggacagagacaacaagca 915 	SOURC	URCE human liver. ORGANISM Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin!; Hominidae; Homo.
caaccetgagatatgeteteetteteetgetgaageaeceagagsteaeagetaaagtee 975 	AUTHORS AUTHORS TITLE	

Oy 583 aattottaacttgatggaaaaattgaatgaaaacatcaggattgtaagcacccctgga 642	Oy 103 tacttaaaaaccttgcttttatggaaaqtgatatttiggagaaagtaaaagaacaccaag 762 Db 661 TACTTAAAAGTIGCTTTTATGAAAATTATATTTGGAAAAGTAAAAGAACACCAG 720 Oy 763 aatcgatgaacatcaacaaccttgggaactttattgattg		1003 gaaaccggagccccqcaqqqccacqqqqqqccacqqqccqcqqqqqqqq	0y 1123 acqtisaatcaqtcatcctcattcccabggcacaaccatattaacttccctcactt 1182 10 1	0y 1243 tggatgaagttggaaattttaagaaaagtaactacttcatgcctttctcagcagaaaac 1302 1201 TGGATGAAGTGCGAATTTTAAGAAAGTAAATCTTCATCACCTTTCTCAGCAGGAAAAC 1260 0y 1303 ggatttgtgtgggagggcctggcccgcatggagctgtttttattcctgaccttcattt 1362 0y 1303 ggatttgtgtgggagaggcctggcccgcatggagctgtttttattcctgaccttcattt 1362 0b 1303 GGATTGGTGGGAAGCCTGGCCGCGAGGACTGTTTTTTTTT	0y 1363 tacagaactttaacctgaaatctctgattgacccaaagaaccttgacacaactcctgttg 1422 1321 TACAGAACTTTAACCTGAAATCTCTGGTTGACCCCAAAGAACCTTGACACCACTCCAGTTG 1380 0y 1423 tcatgatttgcttctgcccccttcatcacgctggttcattcctgctcaaagaa 1462 0y 11423 tcatgatttgcttcttgccccccttcatcaacgtggttcaatcctgctcaaagaa 1462 0b 1381 tCAAIGGATTIGCCTCTGTGCCGCCTTCTACCAGCTGTTCAATCCTGTGTGAAAA 1440	0y 1483 gracagalggtctggctgctctgtgctgtcctggggctctcttcctctgg1535 bb 1441 Gardatgcctgcctgctgctgcarcctgtgarcarctctrctct
JORNAL Blochem Int. 27 (5), 1073-1081 (1992) MEDLINE 9107524. REDARK Genbank staff at the National Library of Medicine created this entry (MERI glubsq 117179) from the original journal article. This sequence comes from Fig. 1. COMMENT Author also gives sequence for another cytochrome P-450 that contains a 6-base deletion of nucleotides 783-788. FEATURES Location/Qualifiers	tens" 6" 22C9 gene" 22C9 gene"	/note="This sequence comes from Fig. 1" /codon: \$tart=1" /codon: \$tart=1" /codon: \$tart=1" /product="cytochrome p-450" /protein_di="Am821864.2" /db_ref="Gi:505937" /d	MEDPHIFLDEGGHEKKSFYERPESAGREICVGEALAGMELFLELTSILONFNILKSI. S17 a 413 c 369 9 515 t 85.74; Score 1495.8; DB 9; Length 1814;	1597; Conservative 0; Mismatches 107; Indels 17; Gagtificational conservative 0; Mismatches 107; Indels 17; Gagtificational content of the co	163 cottaaccaatctctcaaaaatctattgccctgtgttcactcgtattttggcctggaac 163 cottaaccaatctctcaaaaatctattgccctgtgttcactcgtattttggcttggaac 161 1111111111111111111111111111111111		403

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# 15-JUL-1994 JP 94P 194P 194P 194D 194P 196053
# 17-JUN-1994 JP 94P 194P 194P 196053
# RAPEAR KOLISARAN TOSHIYUKI, YABUSAKI YOSHIYASU,
# KANEN HODEN, NAKATSURA 114AO
# C1201/02-C17aM/134,C1201/26;
# KANEN GOGGES: Double:
# C1201/02-C17aM/134,C1201/26;
# C1201/03-C17aM/134,C1201/26;
# C1201/03-C17aM/134,C1201/
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1. .1473 / Arganism-"Homo sapiens"
1. .1473 / Product-"human cytochrome P450 2019"
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02-SEP-2000 (Rel. 65, Last updated, Version
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/db_xref="taxon:9606"
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1. (Dases 1 to 2395)
Scomkes, M. Faletto, M. B., Bialsdell, J. A., Raucy, J. L. and Coldatein, J. A., Faletto, M. B., Bialsdell, J. A., Raucy, J. L. and Coldatein, J. A.

Correction: Cloning and expression of complementary cDNAs for multiple members of the human cytochrome P450IC subfamily
Biochamistry 32, 1390-1390 (1993)
Biochamistry 32, 1390-1390 (1993)
Biochamistry 32, 1390-1390 (1993)
Resequencing demonstrated that it is not a separate gene under Accession Number M61888
Resequencing demonstrated that it is not a separate pere, but is a splice variant or a composite cDNA. The 5' portion corresponds to a partial 2018 clone, and the 3' portion corresponds to a partial 2018 clone.

The 5' end from 10 931 corresponds to a partial allelic variant of 2018 beginning a base fall of 2018 concinuing through base pair 1039 canding for 11e 129 instead of Met 129 and 8 to A change at 387 coding for 11e 129 instead of Met 129 and 8 to A change at 187 coding for 11e 129 instead of Met 129 and 6 to A change at 187 coding for 10131 instead of Met 129 and 6 to A change at 187 coding for 10131 stated of Met 129 and 6 to A change at 187 coding for 10131 stated of Met 129 and 6 to A change at 187 coding for 10135 instead of Met 129 and 6 to A change at 187 coding for 10135 instead of Met 129 and 8 to A change at 187 coding for 10135 instead of Met 129 and 8 to A change at 187 coding for 10135 instead of Met 129 and 8 to A change at 187 coding for 10135 corresponds to a partial 2019 clone through base pair 1612.
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Human cytochrome P4502C18 and P4502C19 splice variant or composite
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an A to G substitution at 991 of 2C19 coding for Gln335 instead of
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/product-'human hepatic cytochrome P450 FT 2C19-derived
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548 TGAATGAAACACTGGAATGTAAGCACCCCTGGATCCAGAATAATTTTCCA 607
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    1444
/organism='Artificial sequences' FT

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BADA.T., KITICAS, and ADVAMB.J.
BADA.T., KITICAS, and ADVAMB.J.

MAGS EXPRESSION STSTEM OF MODIFIED SUBSTANCE OF CTOCHRONE P450 2C15
IN ESCHERICHIA COLI
SPECIAL: JP 1998031166-A 1 10-FEB-1998;
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human hepatic cytochrome P450 2C19-derived
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Db 788 ANTICACTATTGAAAACTTGGTAATCACTGCAGCTGACTTACTT	1207	1327 cccgcatggggctgttttattcctggccttcattttccggaacttcacccggaactt 1268 cccgcatggggctgtttTtATTccTgaccttcatTTTAccGACCTGAAATTCT 1387 tgattgacccaaaggaccttgaacacctgttgtcattgtcattctcttcccgc 1387 tgattgacccaaaggaccttgaacacctgttgtcaatgtatttctctctc	447 ccttctatagetggettcattccrgrct, 11	SOURCE Human liver, CDNA to mRNA, clone MP-8. SULATIVES GEOGE BULL STATE STAT	source 1. 1377 / Organism-Homo saplens' / Ab_aref-"taxon:9606" / // // // // // // // // // // // //

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19 1373.6 78.7	§ §
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545.2 37.0 1356	
627 4 35 9 1479	
637 3 35 0 1403	{
627.2 35.9 1482	
35.9 1482	2
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RESULT 1	
AAV44153	
	45 B
DE Human cytochrome P450 2C19 clon	clon
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XX 22	
## April 19, 2002, 07:21:40; Search time 277.57 Seconds 15.000	

ALIGNMENTS

					SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	80	ID	Description
-	1739.6		1746	13	AAV44153	Human Cytochrome
7	1739.6	9.66	1748	22	AAD12241	Human cytochrome
•	1738		1746	17	AAT03708	Cytochrone 9450 20
-	1632.4		1669	19	AAV12759	Wild type cytochro
'n	1534.6	87.9	1845	50	AAX19925	Mamma I ian cytochro
\$	1534.6	87.9	1852	17	AAT11381	Cytochrome P450 20
7	1534.6	87.9	1852	13	AAV44157	Human cytochrome
œ	1529.8	87.6	1854	17	AAT11378	Cytochrome P450 20
6	1529.8	87.6	1854	19	AAV44154	Human cytochrome
10	1458.6	83.5	1473	16	AA087728	Human auxillary
11	1458.6	83.5	1473	17	AAT28394	Ruman cytochrone

RESULI	
AA	AAV44153
10	AAV44153 standard; cDNA: 1746 BP.
×	
AC.	AAV4153;
××	
IG	06-OCI-1998 (first entry)
×	
ЭE	Human cytochrome P450 2C19 clone 11a cDNA.
X	
×	Cytochrome P450; druq screening; S-mephenytoin 4'-hydroxylase;
E N	identification; mutagenic carcinogenic cytotoxic; haemoprotein;
X	xenobiotic; environmental pollutant; ss.
×	
SO	Homo sapiens.
×	
Z.	US5786191-A.
X	
PD	28-JUL-1998.
×	
<u>د.</u> ۵.	22-FEB-1994; 94US-0201118.
×	
PR	22-FEB-1994; 94US-0201118.
P.R	09-APR-1992; 92US-0864962.
×	
¥d.	(GOLD/) GOLDSTEIN J A.
ΡA	(ROMK/) ROMKES-SPARKS M.
×	
ы	Goldstein JA, Romkes-sparks M;
X	
DR	WPI; 1998-436528/37.
XX	
14	Screening for drugs metabolised by cytochrome P450 - for identifying
ΡŢ	mutagenic, carcinogenic, or cytotoxic compounds

us-09-763-292-1.rng

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Example 2; Column 35-38; 63pp; English
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	09 841	Db 841	0y 901	Db 901	Qy 961	Db 961	Qy 1021	Db 1021	Oy 1081	Db 1081	0y 1141	Db 1141	Oy 1201	Db 1201	0y 1261	Db 1261	Oy 1321	Db 1321	Oy 1381	Db 1381	Oy 1441	Db 1441	0y 1501	Db 1501	Qy 1561	Db 1561	Oy 1621	Db 1621	Oy 1681	DP 1681	Oy 1741	Db 1741	RESULT 2	2241 AAD1	XX AC AAD12 XX	
Example 2; Column 35-38; 63pp: English.	This sequence encodes a cytochrome P450 2019 polypeptide isolated	from human clone 11a. This polypeptide is used in a method to screen for a drug that is metabolised by a cytochrome P450 having S-mephenytoin		large family of haemoprotein enzymes capable of metabolising xenobiotics such as drugs carcinogens and environmental molitaries as well as	endobiotics such as steroids, fatty acids and prostaglandins.	Sequence 1746 BP; 477 A; 418 C; 365 G; 486 T; 0 other;	Match 99.6%: Score 17	No. 0; Lindels 0;	atcettttataateettataetetetetetetetetetet		tetanaanaanatetanaanaanaanaanateenteente	tetggagacagagetetgggagagagaaaaeteeetetggeeeeteeteteeatga 12	-		74		30		· ·				-		ccaaggettcacctqtgatccactttcatcctgggctgtgctcacatgtactc54	481 ccaaggettcaccetqtqatccacttcatcctqqctqqctqqctccctccatqqtct 540	9		aaaaattgaatgaaaacatcaqqattgtaagcacccctgqatccaqatatgcaatat	· · ·		ttccactatcattgattatttcccgggaacccataacaaattacttaaaaaccttgctt 72	aaaqtqatattttqqaqaaaqtaaaqqaacaccaaqaatcqatqqacatcaa	11111111111111111111111111111111111111	781 acceteggaetttottgattgetteetgatesaaatgagaaggaaaggaaaaccaac 840	

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đ	1321		1380
ò	1381	aatctetgattgacccaaaggacettgacacaactcctgttgtcaatggatttgettctg	1440
Д	1381		1440
οy	1441	tecegeettetateagetgtgetteatteetgtetgaagaageacagatggtetggetg	1500
đ	1441		1500
ογ	1501	ctcctgtgctgtccctgcagctctctttcctctggtccaaatttcactatctgtgatgct	1560
đ	1501		1560
Οy	1561	tettetgacegteateteaeatttteeetteeecaagatetagtgaacatteageete	1620
Q	1561		1620
o,	1621		1680
Q	1621	cattaaaaaaytttcactgtgcaaatatatctgctattccccatactctataatagttac	1680
ò	1681	attgagtgccacataatgctgatacttgtctaatgttgagttattaacatattatta	1740
đ	1691		1740
o,	1741	aataga 1746	
Ω	1741	aataga 1746	
RES AAI ID	RESULT 2 AAD12241 ID AAD12241	2 2241 standard: cDNA, 1748 BP.	
* 4 *	AADI	AAD12241;	

us-09-763-292-1.rng

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Ruman; gene structure; phenotypic expression; guanosine cofactor;
germine variation analysis; axon-intron boundary; Tetrahymena rRNA;
cytochrome P450 ZC19; CF1450 ZC19; ss.
                                                                                                                                                      Location/Qualifiers
8 ..10
/*tag a /note 'Translation start site'
40 ..59
/*tag b /*tag b //bound_molety* 'Primer 40L'
complement (43 ..57)
/*tag c
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192...13
192...13
/*tag- g
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/*tag= u
                               Human cytochrome P450 (CYP450) 2C19 cDNA
25-SEP-2001 (first entry)
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misc_signal
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Determining structure of genes whose sequence is not known from cDNA, by sequencing the gene or gene across exon intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the CDNA of gene /bound_moiety- 'Primer 10640'
/'tag- 'x
/'bound_moiety- 'Primer 11061'
/'cag- x
/'tag- x
/'bound_moiety- 'Primer 11080'
/'tag- x
/'tag- y
/'bound_moiety- 'Primer 11080'
/'ag- y
/'bound_moiety- 'Primer 11080'
/'couplement (1215.1129)
/'couplement (1215.1129) /*tag ae Couplement (1700..1317) /*tag a f /*Cound_moiety **Primer 15700** /bound_molety= "Primer 1063L" complement (1064..1079) Dound_molety= "Primer 1231U" [238..1259 ^*tag= aa /bound_molety- *Primer 1238L*
complement (1420..1439)
/*tag- ab
/bound_molety- *Primer 1396U*
1422..1443 /*tag= ac /bound_moiety= "Primer 1392L" complement (1549..1568) /*tag= ad //bound_mojety= *Primer 1519U* /*tag- ag /bound_moiety- "Primer 1690L" (GENO-) GENOME THERAPEUTICS CORP. 17-JAN-2001; 2001WO-US01451. 20-JAN-2000; 2000US-0488127 Thomann H, Fitzgerald MS: WPI; 2001-465380/50. WO200153529-A2. primer_bind 26-JUL-2001. primer_bind primer_bind

The present invention relates to a method for determining gene structure when the genomic sequence is unknown. The method involves structure when the genomic sequence is unknown. The method involves sequencing the gene across exon-intron boundaries using evenly spaced primers or tiled primers. The tiled primers competies motivate across the form of the Example 2; Fig 3; 81pp; English.

961 tcacagctaaagtccaggaagaattgaacgtgtcattggcagaaccctgca 	1081	111 IIII IIIII IIII IIII IIII IIII IIII IIII IIII IIII IIIII IIII IIII IIII IIII IIII IIII IIII IIII IIIII IIII IIII IIII IIII IIII IIII IIII IIIII IIIII IIII IIII IIII IIII IIII IIII IIII IIII IIIII IIIII IIIII IIIIII	1203	1263	1323	1983 aatetetgattgacceaaaggacettgacacaactetytytytytytytytytytytytytytytytytytyt	1443 tecegrecticialcagegggetteattectgettgaagaagaagaagagggggggggg	1503 ctockytytytellillillillillillillillillillillillilli	156 tetrogaccogreatereatticecteceaageriagecoccitifili	162] cattaaaaaagtttcactgtgaaatatatctgctattccccatactci	1683 attgagtgcacataatgttgatacttgttaatgttgagttattacatattatta 1711)y 1/41 abigga 1/46 Db 1743 aataga 1748	EESULT 3 AAI03708 IV AAI03708 standard; CDNA: 1746 BP.	XX AAT03708; XX	E Cytochrome P450 2C19 cDNA. KX K Cytochrome P450 2C19; human; liver; PCR: primer; detection; K etracensorific s-menhanicin 1 -hvdrowebase ariivity: nolymorphism; ss.	Homo saplens.
6 6 6 6 	8 8 8 8	S 8 S	6 G	9 %	e 8	S & S	ස් සි ද්	5 B	. a	Oy.	da da	oy da	AAI	SAXEX		×0×
CC furthe presence of guanosine cofactor. The present sequence is human cytochtrome P450 (CTP450) 2219 cDNA related to the invention. XX SQUECTION SEQUENCE 1748 BP; 478 A; 419 C; 365 G; 486 T; 0 other; QUETY MATCH GUETY GUETY	Oy 1 ctrcaatggatccttttgtggtccttgtgtctctcatgtttgcttctccttcaa 50	61 tctggagacagagctctgggagagaaactccctcctgggcccactcctctcccagtga 1	 121 ttggaatatcctacgatagatattaaggatgtcagcaatccttacccaatctctcaa 	181 aaatetatggcetgtgtteactetgtattttggeetggaeggaeggetggetg 	Oy 241 gataqqaaqqaqqaaqqaaqqaaqqaaqqaaqqaqqaaqqaqqqaqqqaqqqaqqqq	Oy 301 attroccartggctgaaagagtaacagagatttggaatcgtttcagcaatggaaaga 360	Oy 361 gatggaaggagattcggcgtttctcctcatgacgctgcggaattttgggatgggaaga 420 	Oy 421 ggagcattgaggaccgtgttcaagaggaagccgctgccttgtggaggagttgagaaaaa 480 	Oy 481 ccaaggetteaccetgtgatcccacttcatcctgggctgtgctccctgcaatgtgatct 540	Oy 541 gctccattattttccagaaacgtttcgattataaagatcacgaatttcttaacttgatgg 600	Oy 601 aaaaattgaatgaaacatcaggattgtaagcaccccttgatccagatatgcaataatt 550	Oy 661 trocoactateattgattatttcccgggaacccataacaaattatttaattaa	Oy 721 ttatggamagtgatetttggagamagtamaggamcaccagamatcgatggacatcamca 780 	Oy 781 accrtoggactttattgattgcttcctgatcaaatggagaaggaaaagcaaaccac 840	Oy · 841 agtctgaattcactattgaaaacttgqtaatcactgcagctgacttacttggagctgga 900 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 901 cagagacaacaagcacaaccctgagatatgctctcttctctgctgaagcaccagagg 950

```
ochrome P450 2C19; human; liver; PCR; primer; detection;
reospecific S-mephenytoin 4<sup>-</sup>hydroxy<del>lame</del> activity; polymorphism; ss.
1 tettetgacceteateteaeattteeetteeecaaatetagigaaeatteageete 1620
                                                                                                                                                  3 tettetgaccogteateteacattttecettececeaagatetagtgaacatteageete 1622
                                                                                                                                                                                                                                                                                                                                             03708 standard; cDNA; 1745 BP.
                                                                                                                                                                                                                                                                                                                                                                                              SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    ochrome P450 2C19 cDNA.
                                                                                                                                                                                                                                                      1 aataga 1746
                                                                                                                                                                                                                                                                              aataga 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o sapiens.
                                                                                                                                                                                                                                                                                                                                                                      03708;
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This sequence encodes the cytochrome P450 2C19 and was isolated from a human liver CNRA library. 2C19 proteins exhibit stereospecific S-compehenytoin 4-hydroxylase activity, with a typical activity of at least I manol mephenytoin per man of 2C19 per min. 2C19 is thought to be the principal human determinant of this activity in the 2C19 gene contains polymorphisms at nucleotides 636 and 681 of the genomic coling sequence. These can be detected using specific PKE primers which ether amplify the wild type or the mutant altele but not both. These mutations cause the polypeptide to lack substantial shockbarytoin 4-hydroxylase activity, however the phenotype in most individuals which lack S-mephenytoin 4-hydroxylase activity. So casults from a complete or substantial absence of 2C19 polypeptide.

2C19 can be used to identify drugs metabolised by S-mephenytoin C - hydroxylase activity which should not be administered to individuals with a deficiency in S-mephenytoin 4' hydroxylase activity.
                                                                                                                                                                                                                                                                                                                                                            New isolated cytochrome P450 2C subfamily member - used for identifying drugs metabolised by 5-mephonyoin 4'-hydroxylase activity and to develop other screening assays
                                                                                                                                                                                                                                                                     De Morais SMF, Goldstein JA, Romkes-Sparks M;
Location/Qualifiers
6..1478
7*tag- a
/product- Cytochrome P450 2C19
                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 92-93; 169pp; English.
                                                                                                                                                                                                94US-0238821.
                                                                                                                                                            95WO-US05744.
                                                                                                                                                                                                                                                                                                       WPI 1996-077257/08.
P-PSDB: AAR88329.
                                                                                                                                                                                             06-MAY-1994;
                                                                                      W09530766-A1.
                                                                                                                                                            08-MAY-1995;
                                                                                                                        16-NOV-1995.
    Key
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Sequence 1746 BP; 477 A; 417 C; 365 G; 487 I; 0 other.

		2	TD Apr regeade	9
y Match	99.54;	c).	1021 tgcacga	w —
Local hes 174	Local Similarity 99.7%; Pred. No. 0; hes 1741: Conservative 0: Mismatches 5: Indels 0: Gans 0:	qq	1021 tgcagga	ro
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Claim 11; Page 11-12; 15pp; Japanese
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Cytochrome P450 2C19; human; uninterrupted metabolism; omeprazole; diazepam; imipramine; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aa:Asn)
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aa:Asn)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
33..1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wild type cytochrome P450 2C19 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV12759 standard; cDNA; 1669 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96JP-0193015.
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P-PSDB; AAW41161.
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This sequence represents the wild type human liver derived cytochrome P450 ZC19 agene. Modified versions of the encoded protein are the proteins of the human in a cid with Ala and a deletion of amino acid residues 3-20 of the main or acid residues 3-20 of the vill type. Modified cytochrome P490 ZC19 is useful for, uninterrupted whusto.
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208 amaictalgyccrtgigitcartcigiaittiggancganaganggiggiggiggig 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 93.5%: Score 1632.4; DB 19; Length 1669; Best Local Similarity 99.6%; Pred No.0; Asches 168; Conservative 0; Mismatches 6; Indels 0; Conservative 0; Mismatches 6; Conservative 0; Conservative 0; Conservative 0; Conservative 0; Conserv
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cytochrome P450 protein. The fusion protein can oxidise hydrocarbons or any compound having a carbon-hydrogen boad. The fusion protein can be used for hydroxylating a compound to be oxidised. It can also be used be the bloremediation of an environmental pollutant. Since the fusion protein is soluble. It can be subject to structural elucidation by X-ray exptailography for designing functional proteins. It can be readily expressed in soil bacteria to facilitate bloremediation. The present sequence encodes mammalian cytochrome PATO protein CYP209 from the
                                                                                                                                                                                    invention describes a fusion proteins comprising a portion at cytochrome P450 protein and also a portion of a mammalian
                                                                                                                                                                                                                                                                                                                                                                                       61 tetggagacagagetetggagagaaactecetecteggeeceactecteteceagtga 120 [11]]]]
                                                                                                                                                                                                                                                                                                                                                                                                    121 ttggaaatatectacagatagatattaagaatgteageaatecttaaceaatectetea 180
                                                                                                                                                                                                                                                                                                                                                                                                                                    101 aaatctatggcctgtgttcactctgtattttggcctgaacgcatggtggtgctgcatg 240
186 aggtctatggcctggtcactcgtattttggccgaacccalagggcgcgatg 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 gatatgaagtggtgaaggggggggttgatcttggagaggggttttctggaagaggcc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccaaggetteaccetgtgateceaettteatectgggetgtgetecetgeaatgtgatet 540
                                                                                                                        New P450 fusion proteins - comprising a portion of a bacterial cytochrome P450 protein and a portion of a mammalian cytochrome P450 protein
                                                                                                                                                                                                                                                                                                                     Score 1534.6; DB 20; Length 1845;
Pred. No. 0;
0; Mismatches 109; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                     Sequence 1845 BP; 507 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                                                   Disclosure; Page 10-11; Slpp; English
                                                                                                                                                                                                                                                                                                                     Query Match 87.9%;
Best Local Similarity 92.9%;
Matches 1637; Conservative
                                     98WO-DS16979
                                                    97US-0056754
                                                                                                                                                                                                    cytochrome P450 protein.
                                                                      (UYRP ) UNIV ROCHESTER.
                                                                                       Jones JP, Shimoji M;
                                                                                                        WPI; 1999-190131/16.
P-PSDB; AAY04127.
                                                                                                                                                                                                                                                                            present invention.
                                    17-AUG-1998;
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   WO9908812-A1
                   25-FEB-1999.
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1288 ttaagaaaagtaactactcatgcttctcagcaggaaaacggattggtgggaggg 1347
                                                                                                                                                                                                                                                                                 Bacterial: mammallan; cytochrome P450; chimeric; fusion protein: oxidise; hydrocarbon: carbon-hydrogen bond; hydroxylating; bioremediation; environmental poliutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian cytochrome P450 protein CYP2C9 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX19925 standard; DNA; 1845 BP.
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1566 taatgccttttctcacctgtcatctcacatttcccttgaagatctggtgaacatt 1625 1614 cagcctccatta	RESULT 6 AAT11381 standard; CDNA; 1852 BP. AAT11381 standard; CDNA; 1852 BP. AAT11381; O9-SEP-1996 (first entry) E Cytochrome P450 2C9 clone 65 coding sequence. Cytochrome P450 2C9; human: liver: PCR; primer; detection: CYP2C19; XX Cytochrome P450 2C9; human: liver: PCR; primer; detection: CYP2C19; XX Cytochrome P450 2C9; human: liver: PCR; primer; detection: CYP2C19; XX Cytochrome P450 2C9; human: liver: PCR; primer; detection: CYP2C19; XX Homo sapiens. XX Homo sapiens. XX Hory Cytochrome P450 C9 clone 25 FFT CDS 11148 FFT CDS 11149 FFT CAPE CO	
40 40 40 40 40 40 40 40 40 40 40 40 40 4	#¥	38888
	721 (tatggaaagtgatattttgagagaaagtaaaagaaacccaagaatcgatggacatcaaca 780 726 (tatggaaagtgatattttgagagaaagtaaaaggaacccaagaatcgatggacatgaca 726 (tatggaaagtaaattttgattgattgatttactgattacaaatgagaaaccaaggaaccagaca 781 accttgggactttatttgattgattgattccgatcaaaatgagaaaccaaggaacagaca 781 accttgggactttattgattgattgattccgatcaaatgagaacccaaggaaccaacc	1506 etgetygtgegteeteggageteletteetelggggaattatedaletteatate; 1555 1554 tgatgeftettetgggeegteateteeseattteeetteeetaggaatat 1513

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Clone
polyadenylation signal 21 bases from the poly-A tail.
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946 901 961 966 1021	1081 togacctatccaecoacquiquecottqacquiquecitygagqtaaktcaaaatcaaaadt 11111	0y 1201 aagaatticccaacccagaatgitigacctigtcactititggatgaaggiggaaatt 1260 1206 aagaatticccaacccagagatgitigaccticatcactititgatgatgaaggiggcaatt 1206 aagaatticccaacccagagatgitigaccticatcactititgatgatgaaggiggcaatt 1206 is aagaaataactaticatgictititicagaggaaaacggattigitgiggagagag 1306 is taagaaaagtaaatacticatgictiticagaggaaaacggattigitgiggagagag 1206 is taagaaaagtaaatacticatgictiticagaggaaaacggattigitgigggagag 1206 is aagaaaagtaaaatacticatgictiticagaaggaaaacggattigitgigggagagg 1206 is aagaaaagtaaaaacticatgictiticagaaggaaaacggattigitgigggagaag 1206 is aagaaaagtaaaatacticatgictiticagaaggaaaacggattigitgigggagaag 1206 is aagaaaagtaaaatacticatgictiticagaaggaaaacggattigitgigggagaag 1206 is aagaaaagtaaaatacticatgictiticagaaggaaaacggattigitgigggaaaggaaa	0y 1321 gectggccegcatggagctgttttattcctgaccttcatttaccagaactttaacctga 1380 clr[] [] [] [] [] [] [] [] [] [] [] [] [] [1446 1501 1506	155 tatgetcetcactgaccetcacttcettcettcettcettatggacatt 156 tatgctttctcacctgtcatctcactttccttccttgaagatctatggaacatt 156 tatgcttttctcacctgtcatctcacatttcccttccttgaagatctatggaacatt 1614 cagcctccattaaaabagtttcactgtgcaaatatatctgctattcccc 1614 cagcctccatta	decterateateateateateateateateateateateateatea	### ### ### ### ### ### ### ### ### ##
8 6 8 6 8 8	94 90 90 90	0 0 0 0	O A O Ā	0 0 0 0			
cc and a polyadenylation signal 21 bases from the poly.A tail. Clone 5b cc has an unusually long 3'-noncoding region containing three possible cc polyadenylation signals with no poly.A tail. The differences in the 3' cc ratiants, or possibly separate genes. These clones are designated as a liellor variants of 2C18 because they differ by only one base in the cc coding region. They are most similar to 2C9 (82% amino acid homology). XX So sequence 1852 BP; 514 A: 424 C; 380 G; 534 T; 0 other; Ouery Match 87.9%; Score 1534.6; DB 17; Length 1852; Bast Local Similarity 92.9%; Pred. No.0, 109; Indels 17; Gaps 2: Matches 1637; Conservative 0, Mismatches 109; Indels 17; Gaps 2:	1 cttcmatgatcctttgggtccttggctctgctctctatgttgcttctctttcaa 	66 tetggagacagagctetgggagagaaactccctcctggcccactcctcccagtga 121 ttggaaatatcctacagatagatattaaggatgtcagcaatccttaaccaatctctca 121 ttggaaatatcctacagatagatattaaggatgtcagcaatccttaaccaatctctca 126 ttggaaatatcctacagatagtattaagcactcgaaatccttaaccaatctctcaa 181 aaatcatggccctgtgttactctatttgccttgaaagcatggtggtggtgctg 181 lillillillillillillillillillillillillil	186 241 246 301		Oy 481 ccaaggcttcacctgtgatcccactttcatcctggctgtgctcccgcaatgtgatct 540 111111	Oy 601 aaaaattgaatgaaacatcaggattgtaagcacccctggatccagatatgcaataatt 660	Oy 721 ttatggaaagtgatattttggaaaagtaaaagaacaccaagaatcgatggacatcaaca 780

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tochrome P450 2C9 clone 65 cDNA.
                                                              standard: cDNA: 1852 BP
                                                                                 998 (first entry)
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                                                                                                                                                                                                                                                                                                                      This sequence encodes a human cytochrome P450 2C9 polypeptide isolated from clone 65. This polypeptide is used in a method to screen for a drug that is method; listed by a cytochrome P450 having S-mehenytoin 4. ** ***Mycroxylase activity. The protein can also be used to identify a mutagento, carcinogenic or cytochrome compound. Cytochrome P450 are a large family of hamoprotein enzymes capable of metabolishing xenoblotics such as druggens and environmental pollutants as veil as endoblotics such as steroids; fatty acids and prostaglandins.
                                                                                                                                                                                                                                                                Screening for drugs metabolised by cytochrome P450 - for identifying mutagenic, carcinogenic, or cytotoxic compounds
                Cytochrome P450; drug screening; S-mephenytoin 4'-hydroxylase; : identification; mutagenic; carcinogenic; cytotoxic; haemoprotein; recobiotic; environmental poliutani; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1852 BP; 514 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                                                                                                                                                                                   Example 2; Column 53-56; 63pp; English.
                                                                                                                                                                                                                        Goldstein JA, Romkes-sparks
                                                                                                                                                    94US-0201118.
92US-0864962.
                                                                                                                                94US-0201118.
                                                                                                                                                                                      (GOLD/) GOLDSTEIN J A. (ROME/) ROMES-SPARKS H.
                                                                                                                                                                                                                                            WPI; 1998-436528/37.
                                                                                                                                                    22-FEB-1994;
09-APR-1992;
                                                                                                                              22-FEB-1994;
                                                             Homo saplens.
                                                                                   US5786191-A.
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ò qq ò g ò qq 0.7 g õ g ò a o, q ; 121 tiggamatatoctacagatagatattaaggatgicagcamatocttaaccaatctcicaa 180 [11] [11] [11] [11] [11] [11] [12] [13] tiggamatatoctacagataggatataaggacatcagaaatcoctaaccaatctcicaa 185 361 galggaaggagatleggegtlectecteatgaegetgeggaatltegggalggaaag 420 [http://www.new.ac.d.com/ac 245 **341 gatatgaagtggtgaaggaagccctgattgatcttggagaggagttttctggaagagcc 300** 146 gatatgaagcagtgaaggaagccctgattgatcttggagaggagttttctggaagaggca 305 30] atttcccactgctgaaagagctaacagagatttggaatcgttttcagcaatggaaaga 360 421 ggagcattgaggaccgtgttcaagaggaagcccgctgcttgtggaggagttgagaaaaa 480 1 cttcaatggatccttttgtggtccttgtgctctgtctctcatgtttgcttctccttcaa 60 Ouery Match 87.94; Score 1534.6; DB 19: Length 1852; Best Locas Similarity 92.94; Pred. No. 0; Mexches 1637; Conservative 0; Mismatches 109; Indels 17: Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                 Score 1529.8; DB 17; Length 1854;
Pred. No. 0;
0; Mismatches 112; Indels 17; (
                                                                                                                                                                                                                                                           Sequence 1854 BP; 513 A; 424 C; 381 G; 536 T; 0 other;
                                                                                                                                                                                                                                                                                                                         Query Match 87.6 Best Local Similarity 92.7 Matches 1634; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome P450 2019; human; liver; PCR; primer; detection: CYP2019; stereospecific S-mephenytoin 4'-hydroxylase activity; polymorphism: ss.
                                     1614 cagcetecatta------aaaaagtteacttgcaaatatatetgctatteecea 1663 | 1614 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 
                                                                                                                                                                                                                           etgetgtgcagtccctgcagctctctttcctctgggggcattatccatcttcactatctg 1565
                                                                                                                                                                                                1664 tactetataatagttacattgagtgecacataatgetgataettgtetaatgttgagtta 1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mew isolated cytochrome P450 2C subfamily member - used for identifying drugs metabolised by S-mephenytoin 4'-hydroxylase activity and to develop other screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= Cytochrome P450 C9 clone 25
1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Romkes-Sparks M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytochrome P450 2C9 clone 25 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag- b
/note- Variable position"
1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag- c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualiflers
13..1485
                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldstein JA,
                                                                                                                                                                                                                                                                                                                                                                                                                         AA-11378 standard; cDNA: 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US05744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9405-0238821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR89862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09530766-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-1996
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results in one amino acid difference at position 359, lle to Leu. The clones 29c and 6b differ by one nucleotide in the coding region, position 1154. Which results in a single amino acid change. This to Met at position 185. Clone 25c has a very long, 189 bb. 5'-noncoding region and a polyaderylation signal 21 bases iron the poly. A tail. Clone 6b has an unusually long 3'-noncoding region containing three possible polyaderylation signals with no poly. A tail. The differences in the inon-coding regions could represent alterate splicing, allellic variants or possibly separate genes. These clones are designated as allellic variants of 2C18 because thay differ by only one base in the coding region could may be account the second of the coding regions could represent alternate splicing, allellic coding regions could represent alternate splicing, allellic coding regions could represent alternate splicing, allellic

112; Indels 17; Gaps

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36] galggaaggagatteggegttetecectaagaegetgeggaattttggggaaga 420 308 ttttcccactggctgaaagagctaacagaggatttggaattgtttcagcaatggaaaga 367

getecattattttecagaaacgtttegattataaagateaegaatttettaaettgatgg 600

tteceactateattattteeeqqqaaccataacaaattaettaaaaacettgett 720 668 titciccialcatigatiacticcoggaactcacaacaaattacttaaaaacgiigcii 727

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211 galatgaagtgatgaaggaagccctgaltgalcttggaaggagtttctggaaagagcc 300
218 galatgaaggaggaaggaaggaagcccgaltgalcttggactttggagggggtglttcttggaaggagca 307
                                                                                                                                                          87.6%; Score 1529.8; DB 19; Length 1854;
92.7%; Pred. No. 0;
Live 0; Mismatches 112; Indels 17; Gaps
                                                                                                                                                                        Cytochrome P450; drug screening; S-mephenytoin 4'-hydroxylase:
Rednification; mutaqenic carrimogenic: cytotoxic; haemoprotein;
kenobiotic; environmental pollutant; ss.
            Human cytochrome P450 2C9 clone 25 cDNA.
    06-OCT-1998 (first entry)
                                                                                                                                                          Query Match
Best Local Similarity 92.74
Matches 1634; Conservative
                                                                                        WPI: 1998-436528/37.
                                                            22.FEB-1994;
05-APR-1992;
                                                     22-FEB-1994;
                                 Homo sapiens.
                                       US5786191-A.
                                              28-JUL-1998.
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This sequence encodes a cytochrome P450 2C9 polypeptide isolated from than clone 25. This polypeptide is used in a method to screen for a drug that is metabolised by a cytochrome P450 having S-mephenytoin C-hydroxylase activity. The protein can also be used to identify a mutagenic, carcinogenic or cytochrome palso be used to identify a mutagenic, carcinogenic or cytochaic compound. Cytochrome P450 are a lurge family of haemoprotein enzymes capable of metabolising xenobiotics such as drugs carcinogens and environmental pollutants as well as endobiotics such as steroids, fatty acids and prostaglandins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening for drugs metabolised by cytochrome P450 \cdot for identifying mutagenic, carcinogenic, or cytotoxic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1854 BP; 513 A; 424 C; 381 G; 536 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Column 39-42; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                              Goldstein JA, Romkes-sparks M;
94US-0201118
                                                                              94US-0201118
92US-0864962
                                                                                                                                                                                                                   (GOLD/) GOLDSTEIN J A. (FOMK/) ROMKES-SPARKS M.
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351 gatggaaggagatteggegttteteeteatgaegetgeggaattttgggatgggaaga 420

Db 1448 tyccyccttctaccagctgtgcttcattcctgtctgaagaagagcagatggctggtg 1507 0y 1501 ctcctgtgctgtcctgcagctctttcctctggtccaatttcactatctg 1553	287	A (1474) MAINTON CHEM CO LTD. X (50MO) SURITIONO CHEM CO CO CONTROL OF SURITION CHEM CONTROL OF CO
### ### ##############################	72 tettgaaagqatatttiggaaaagtaaaagaacaccaagaatcgatgaacatcaaca 780 11	1141 acctcatcccaagggacaaccatattactcccccttctggacaagacaac 1147 1150 illillillillillillillillillillillillill

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888888

auxillary species and variants (AAQ87718-32), and yeast NADPH-P450

នឧឧឧឧ	auxiliary species and variants (AANB/118-3f), and yeast NADH-P450 reductase, either as a fused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound, or	Oy 906 acaacaagcaccaaccctgagatatgttctccttctcctgtagcacccagaggtcaca 965
ខម្		966 gctaaagtccaggaagattgaacgtgtcattggcagaaaccggagccctgcatgca
જ	Sequence 1473 BP; 404 A; 352 C; 327 G; 390 T; 0 other;	gctaaagtccaggaagagattgaacgigtcgttggcagaaaccggagccctgcatgcag
5 Å Ì	Query Match 83.54; Score 1458.6; DB 16; Length 1473; Secre Length 123; Secre 1458.6; DB 16; Length 1473; Secre 1454; Conservative 0; Mismatches 9; Indels 0; Gans 0; Matches 1564; Conservative 0; Mismatches 9; Indels 0; Gans 0;	
5 1	Getetgteteteatgtttgettetecttteaatctgg 65	0y 1006 creatcocacacactorcocacacactorcocacacactor 1145
8 8 1	ategatericity agreement and transfer and transfer agreement agreement and transfer agreement and transfer agreement	Cy 1146 attoccaaggeacaaccatattaactcccccattctgrotaacgacaacaaga 1205 1141 attoccaaggacaacaaccatattaactccctcactctgrotacacaagaa 1200 1141 attoccaaggacaaccaacataactccctcactccgrotacacaagacaacaacaaagaa 1200
8 8 8		Oy 1206 tttcccaacccagagatgtttgacctcgtcactttctggatgaggtggaaattttaag 1265
8 8	and accordance of the state of	Oy 1266 aaaagtaactacttcatcagcaggaaaacggatttgtgggggggg
3 B	ctctgtattttggcctcgagcgcatggtggtgctgcatggatat ccctgattgatcttggagaggagttttctggaagaggccatttc	Oy 1326 gecogcatggagetgttttattectqaecttcatttacagaactttaacctgaaatct 1385
දි දි	cctgattg	1386 ctgattgacccaaaggaccttgacacaactcctgttgtcaatggatttgcttctgtccg
음		1381
රි සි	366 aaggagatteggegtteeteeteatgaegetgeggaattitgggatggga	UV 1440 CCCLCCdategerup gygrudantugutuga 1473 Db 1441 cccttctatcagctgtgcttcattcctgtctga 1473
ර් සි	426 attgaggaccgtgttcaagaggaagcccgctgccttgtggaggagttgagaaaaaccaag 485 	RESULT 11 AA128394 ID AA128394 standard: DNA: 1473 BP.
8	486 getteacctgtgateceaettteatectgggetgtgeteectgaatgtgatetgtee 545	AX AAT28394: AX XX XX T11-CCT-1996 (first entry)
8 8	#ttatttccagaaacgtttcgattataaagatcacgaattcttaacttgatgagaaaa	Human cytochrome P45
셤		XX XX KW Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer XW liver; yeast; expression vector; NADPH-P450 reductase; ADH dene promoter
දී දී	606 tigaatgaaaacatcaggattgtaagcacccctggatccagatatgcaataatttccc 555	evaluation; safety: fusion protein; metabolite; detoxification; carcinogenic; ds.
ð	666 actatcattgattatttcccgggaacccataacaaattacttaaaaaccttgctttata 725	OS Homo sapiens. XX XX Py Jp08056695-A.
a	ccataacaaattacttaaaaaccttgcttttatg	
ð 5	726 gaaagtgatattttggagaaagtaaaagaacaccaagaatcgatggacatcaacaacct 785 	15-JUL-1994;
8 6 8	999-6-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	PR 17-JUN-1994; 94JP-013603. PR 20-JUL-1995; 93JP-020120. PR 30-JUL-1993; 93JP-0208279.
8 8	cyygarticallyallycliccityalcaaaakyyayaayyyaagayaaaayidaaaaagacaaadaaqaadaaaaaattaattaaaaaattaataaatcaattaatta	
. B		DR WPI; 1995-182311/19. DR P-PSDB; AAR93181.

Novel method for the evaluation of the safety of a cpd. - using a himm retuctars set to determine whether this methor returned to a carcinogen whether the analyte opt. 1s detoxified or metabolised to a carcinogen

Example 1; Page 47-49; 74pp; Japanese.

The street is a second and the street of the This is the nucleotide sequence of the human cytochrome P450 molecular species 2C19 gene which encodes a protein of 490 mains acids. The gene was amplified from a human liver derived CDNA library as several fragments using primers ANTA5902-22. The prod. was cloned into the

0; Gaps Query Match 83.51; Score 1458.6; DB 17; Length 1473; Best Local Similarity 99.14; Pred. No. 0; Assuches 1461; Conservative 0; Mismatches 9; Indels 0; G

Match	ies	Matches 1464; Conservative 0; Mismatches 9; Indels 0; Gaps	S
ğ	9	atggatccttttgtggtccttgtgtctctcatgtttgcttccctttcaatctgg 65	
å	7		
Š	99	s agacagagetetgggagagagaeetecetectegececactecteceaggatega 125	v
g	61		0
, ,	126	aatateetacagatagatattaaggatgteagcaaateettaaceaateteteaaaate 18	S
9	121		0
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q	181		
Ė	246		2
£	241		0
6	306		2
8	301		0
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8	361		0
6	426		κ
8	431		0
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요	481		0
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æ	541	attattitecagaaacgittegattataaagateagcaatteettaaettigatggaaaaa	600
δ	909	ttgaatgaaaacatcaggattgtaagcacccctggatccagatatgcaataattttccc	555
윰	601	ttgaatgaaaacatcaggattgtaagcaccccctggatccagatatgcaataattttccc	950

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đ	661 8	actatcattgattatttcccgggaacccataacaaattacttaaaaaccttgctttatg 720	0
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ογ	996	ctaaagtecaagaagagattgaacgtgteattggeagaaaceggageeeetgeatgeae 10	25
ф	961	tccaggaagaattgaacgtgtcgttggcagaaaccggagcccctgcatgca	20
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qq	1021	caggggccacatgccctacacagatgctgtggtgcacgaggtccagagatacatcga	86
Qy	1086	tcatccccaccagcctgccccatgcagtgacctgtgacgttaaattcagaaa	5
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οy	1266	aaagtaactacttcatgcctttctcagcagaaaacggattgtgtgggagagggcctg l	
đ	1251	aggtaactacttcatgcctttctcagcaggaaacggatttgtgtgggggggg	320
oy	1326	ccgcatggagctgttttattcctgaccttcattttacagaactttaacctgaaatct 1	38
q		tittattootgacottoatttacagaactttaacotgaatot 1	380
Oy	1386	igattgacccaaaggaccttgacacaactcctgttgtcaatggatttgcttctgtcccg 1	4
đ	1381	aggacettgacacaactcctgttgtcaatggatttgcttctgtccg 1	4
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qq		attectgtetga 147	
	3599 AAQ	is99 standard; DNA; 1818 BP.	
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X G X	Нишаг	ver cy	
¥ 2 2	P-45	0; cytochrome; Saccharomyces cerevisiae; r disorders; ds.	
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271 ggcatttcccactggctgaaagagctaacagagattcggaattgtttcagcaatgg 330
                                                                                                                                                                                                                                                                                                                                                                                                             aagagatggaaggattcggcgtttctccctatgacgctgcggaattttgggatgggg 415
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                                                                                                                                                                                                                                                                                                      gtgattggaaatatcctacagataggtattaaggacatcagcaaatccttaaccaatctc 150
                                                                                                                                                                                                                             83.3%; Score 1455; DB 11; Length 1818;
92.2%; Pred. No. 0;
Live 0; Mismatches 110; Indels 23; Gaps
                                                                                                                                                                          The P-450 produced from plasmid phPA6 in a yeast expression system meterally Sectharomyces AH21, can be used to treat human liver disorders, oxidising various chemical substances.
                                                                                                                              Recombinant plasmid, for yeast for liver treatment - comprises human liver cytochrome P-450MP gene obtd. from yeast,
                                                                                                                                                                                                       Sequence 1818 BP; 516 A; 412 C; 376 G; 514 T; 0 other;
Location/Qualifiers
1..1443
/*tag= a
                                                                                                                                                            Disclosure; Fig 4: 9pp; Japanese.
                                                                                         (AGEN ) AGENCY OF IND SCI TECH.
                                                           88JP-0225955.
                                                                           88JP-0225955.
                                                                                                                                                                                                                               Ouery Match 83.3 Best Local Similarity 92.2 Matches 1574; Conservative
                                                                                                        WPI; 1990-121045/16.
P-PSDB; AAR04043.
                             JP02072879-A.
                                                           09-SEP-1988;
                                                                           09-SEP-1988;
                                            13-MAR-1990
                                                                                                                                                                                                                                                            23
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1497 getgeteetgtgetgteeetgeagetetetteetetgg------tecaaattteaeta 1549 gagtcacagctaaagtccaggaagaattgaacgtgtcattggcagaaccggagccc 1016 tacatogacotcatocococogoctgococògoatgacotqqaoqttaaattoaqa 1136 gagggectggecegeatggagetgttttatteetgaeetttaeagaaetttaae 1376 925 gaggtcacagctaaagtccaggaagaagagttgaacgtgtgattggcagaaaccggagccc 984

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48] craaggettcaccetgigatccacttcatccqqqctqqqctqqqcccqqqaaaqqaatt 540
518 craaggeccacctqqqatccaccttcatccqqqqtqqqctqqqcccqqqaaqqqqctc777
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                                                 241 gataigaagiggigaaggaaggcccigaligatciiggagagagailiciggaagaggcc 300
278 ghillillillillillillillillillillillilli
278 gataigaaggaggaggaaggaaggaagsccigaligaicmggagagaggaggillicitggaagaggca 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this sequence encodes a human cytochrome P450 2C polypeptide. This by veptide is used in a method too screen for a drug that is methodised by a cytochrome P450 having S-mephenytoin 4' hydroxylase activity. The protein can also be used to identify a mutegenic, carcinogenic or cytochrome P450 are a large family of haemoprotein earymes capable of metabolising xenoblotics such as drugs carcinogens and earlingmantal pollutants as well as endoblotics such as steroids, faity acids and prostaglandins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for drugs metabolised by cytochrome P450 - for identifying mutagenic, carcinogenic, or cytotoxic compounds
                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome P450; drug screening; S-mephenytoin 4'-hydroxylase:
Identification; mutagenic carcinosenic; cytotoxic; haemoprotein:
xenobiotic; environmental pollutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1892 BP; 481 A; 396 C; 358 G; 500 T; 157 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 63-66; 63pp; English.
       Human cytochrome P450 2C genomic DNA
                                                                                                                                                                                          AAV44159 standard; DNA; 1892 BP.
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92US-0864962
                                                                                                                                                                                                                                                                                            06-0CT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GOLD/) GOLDSTEIN J A. (ROMK/) ROMKES-SPARKS M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-436528/37.
P-PSDB; AAW64075.
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09-APR-1992;
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ID ANA 41159

ID ANA 41
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961 toacagctaaagtccaggaagasttgaacggtatcattggaagaaaccggaaccccgca 1020 1998 tcacagctaaagtccaggaagaaltgaacgtgaattggcagaaacggagacccctgca 1057 1141 acticaticica aggica caactatta atticaticatici gigitata catgaca aca 1200 [Hilli] [H 1201 aagaattteecaacecaaaqatqtttoaecetegteaetttetggatgaaqtggaaatt 1260 1058 tgcaggacaggacacatgccctacacagatgctgtggtgcacgagntccagagataca 1117 g õ 8 ò g ò 8 ó g ; 181 aaatctatggccctgtgttcactctgtattttggcctggaacgcatggtggtgctgcatg 240 Ouery Match 82.31; Score 1436.4; DB 19; Length 1892; Best Local Similarity 86.31; Pred. No. 0; Matches 1523; Conservative 0; Mismatches 221; Indels 17; Gaps

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                                                                                                               aatetetgattgacccaaggacettgacacaacteetgttgteatggatttgettetg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation of genetically modified cell to produce pigment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetic construct for bacterial production of P450 2C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human: cytochrome P450 2C19 monooxygenase; P450 2C19;
pigment production; indole; dye; cosmetic industry; m
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(UTVA-) UNIV VANDERBILI.
(CALT ) CALIFORNIA INST OF TECHNOLOGY.
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MAP76964 standard; DNA; 8475 BP.

AC AA776964;

MAP76964;

MAP769666;

MAP7696666;

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MAP7
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e capacity to produce a
                pigment in the presence of indole, or a precursor, analogue or derivative of indole, upon expression of the genetic material. Figment from plant or plant material is useful in the dye or cosmetic industry or as commercial tass or as markers for transformation of microbial, plant or animal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ettcaccetgtgatccactttcatcctggctgtgctccctgcaatgtgatctgctcca 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        607 tgaatgaaacatcaggattgtaagcacccctggatccagatatgcaataatttccca 666
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788 aattoactatgaaacttggtaatcactgcagctgactacttggagctgggacagg 847
                                                                                                                                                                                                                                                                                          127 atatectacogatagatattaaggatgteageaaateettaaceaateteteaaaaatet 186
                                                                                                                                                                                                                                                                                                                                                                                                  247 aagtgatgaaggcetgattgatettgaaggaggttttetggaagaaggeettte 306
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                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                DB 22; Length 8475;
                                                                                                                                                     Sequence 8475 BP; 2042 A; 2237 C; 2215 G; 1981 T; 0 other;
                                                                                                                                                                                                                                                     18; Indels
                                                                                                                                                                                                                Score 1415.2;
Pred. No. 0;
0; Mismatches
  or
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Best Local Similarity 98.8
Matches 1426; Conservative
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us-09-763-292-1.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgaatgaaaacatcaggattgtaagcacccctggatccagatatgcaataattttccca 666
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
B1.0%, Score 1413.6; DB 19; Length 1447;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1422; Conservative 0; Mismatches 14; Indels 0; Gaps
                                                                                                                                                                                                                        Modified cytochrome P450 2C19 from human liver - useful for uninterrupted metabolism of therapeutics, e.g. omeprazole
/transl_except= (pos: 1306..1308, aa:Asn)
/transl_except= (pos: 1396..1398, aa:Asn)
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1447 BP; 410 A; 341 C; 322 G; 374 T; 0 other;
                                                                                                                                                                                                                                                                      Claim 4; Page 9-10; 15pp; Japanese
                                                                                                                           96JP-0193015.
                                                                                                56JP-0193015
                                                                                                                                                        (SHIO ) SHIONOGI & CO LID.
                                                                                                                                                                                WPI; 1998-172087/16.
P-PSDB; AAW41160.
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                                                                                                                                                                                              Cytochrome P450 2C19; human; uninterrupted metabolism; omeprazole; diazepom; imipramine; mutein; ss.
caacaagcacaaccetgagatatgctctccttctcctgctgaagcacccagaggtcacag
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                                                                      531 tgaatgaaaacatcaggattgtaagcacccctggatccagatatgcaataattttccca 510
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AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,	q 0	203 AAGICTATGGCCCCGIGIICACTCIGIACTTIGGIICAAAGCCTACTGIGGIGGIACATG 262
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	Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,	3	
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Athersys. Inc.

12.01 Carnege Ave. Cleveland, OH 41115, USA
Tel: 15.413 9936
Fax: 216 15.61 9596
Email: scain@athersys.com
High quality sequence stop: 532.
Location/Qualiflers.

1. 1990anism. Hono sapiens.
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237 a 240 c 181 g 250 L lothers
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125 cTGTDAGCACCAGAGTTAAAGTCAGGAAAGTCAGGAATGAAGGGTGTATTGC 184
125 GTGTDAGCACCAGCAGTAAAGTCAGGAAAGTCAGGAATGAAGGGTGAATGC
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Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott J. Cain
                                 JOURNAL
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Homoson Spiens

Boundard: Craniata: Vertebrata: Euteleostomi: Butaryota: Merazoa; Chordata; Craniata: Vertebrata: Euteleostomi: Butaryota: Merazoa; Chordata; Catarrhini; Hominidae: Homo.

Homosoli: Eutheria; Primates: Catarrhini; Hominidae: Homo.

Harrington: Ju. Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,

Lerins: L., Dahl. T., Thornton, M.; Ramachandran R., Whittington, J.,

Leriner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E.,

and Ducar, M.

Creation of Genome-wide Protein Expression Libraries using Random
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BG198889 G1:13720576
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RESULT 5
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AUTHORS

TITLE

1482 agaacagatggtctggtgttctqtgtgtgtctgtcctgcagttcttttttttgg	Db 124 1GCTGAAGCACCCAGAGGTCACCTAAAGTCCAGGAAGAGATGAACGTGTGATTGGCA 183
Db 665 MARCANATGGCTGCTGCTGTTGTATCCTTCACTTTTTTTTTTT	Oy 1003 gaaaccggagcccctgcatgcatgaggggccaattgcctcaaagstgcttggggc 1062 11
Db 725 ATCCATCTTCACTATCTGTAATGCCTTTTCTCACCTGGTATCTCACATTTTCCTCCCT 784 Oy 1595 cceastctaggaccattcagcctctacttaassastttcattgqca 1543 Oy 11595 cceastcgtacattcagcctctagcatta	Oy 1063 acgasgiccagagatacatcatcatcaccagcagcccatgcaggagctgg 1322 bb 244 GCGAGGTCAGAATACATTGAGCTTGTCCAACCAGCCATGCAGTGAGTG
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Db 845 AAATAATCTGTATTCTCCATACTCTGGAACAATTGCATTGACTGCCAC 893 RESULT 6	0y 1183 ctgtgctacatgacaacaagaatttcccaacccagagatgtttgaccctcgtcactttc 1242
BG217233 802 bp RST36935 Athersys RA BG217233	Oy 1243 tggatgaagtggaaattitaagaaaagtaactactccatgccttctcggcaggaaac 1302
VERSION 867.17233.1 GI:13743254 KETHORDE EST. 67:13743254 SOURCE human.	Oy 1303 geattigrapageagegecigaccgcalgagetgttttattcctgaccttcattt 1362 December 1302 December 1303 Decembe
_	1363 tecagaactttaacctgaaatctctgattgacccaaaggaccttgacacaactcctgttg
AUTHORS Harrington J.J., Patef, B., Rundlett, S., Jackson, P.D., Perry, R., AUTHORS Harrington J.J., Fabriton M., Ramachandran R., Whittington J., Lernert, L., Krashoc, D., Welligott, K., Clark, S., Hays, R., Smith, E., Veloso, M., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.	3423
and Ducar,M. IIILE Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression JOURNAL Nat. Blotechnol. 19 (5), 440 (2001) in press	604 TCAATGGATTTGCCTCTGTGCCGCCCTTCTACCASCTGTGCTTCTTTCCTGTGCGAGAAAAAAAAAA
	684 GACCAGATGGCCTGGCTGCTGCTGCTAGCCCTCTGCAGCCTCTTTTTTTT
320C Carnegle Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596	TCCATCTITCACTATCCTGTATGCTTTTTCTCACGTGTCATCACATTTTTCCTTCC
Enail: scalingthersys.com FPATURES High quality sequence stop: 473. FPATURES 1. 60-00-10-00-00-10-00-00-00-00-00-00-00-00	Oy 1596 coagatctagtgaacattc 1514 Db 784 GACGAICIANTHIITH 00 T84 GACGAICIAGTGAACATC 802
	RESULT 7 805567504 10-APR-2001
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Query Match 38.5%; Score 672.6; DB 11; Length 802; Best Local Similarity 91.1%; Pred. No. 8.3e-173; Matches 728; Conservative 0; Mismatches 64; Indels 7; Gaps 1;	REFERENCE (Dassel to 819) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TILLE National institutes of Health, Mammalian Gene Collection (MGC) JOHNAL Unpublished (1999)
Oy 823 aggaaagcaaaccaacagtctgaatcactatcatacaaactcgacagcugcagcug 882 	COMMENT CONTACT: ROBERT SITUADERGY, Ph.D. Dhall: Capaba-frahl. nih.gov Tissue Procurement: CLONFIER! Laboratories, Inc. CDN Library Preparation: CLONFIER! Laboratories, Inc.
Oy 883 actiactiggagctgggacagacacacacctgagatatgctctctccc 942 1111	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Oy 943 tgctgaagcacccagaggtcacagctaaagtccaggaagagattgaacgtgtcattggca 1002	http://image.lini.gov

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RST18161 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence
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1111 | 111 | 111 | 122 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Watch 35.94; Score 626; DB 11; Length 893; Best Local Similarity 88.44; Pred: NO.4.79-150; Indels 13; Gaps Hatches 727; Conservative 0; Hismatches 62; Indels 13; Gaps
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/note-*See 'Creation of Genome-vide Protein Expression
Libraries using Random Activation of Gene Expression'
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RG19514508 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
BG195327.1 GI:13717014
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301 TTAAATCAAAACTATCCATCCCAAGGCACAACAATATAATTCCTGACTGG 560
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nus mustactus
Enkaryota. Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Hammalas. Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CE 1 (bases 1 Loc 10.7)
Rodera, M. Hiller L., Rucaba, T.; Martin, J., Beck. C., Wylie, T.;
Rarta, H. Hiller L., Steppe, M., The Basing, B., Allen M., Bowers, Y.; Peteron, R., Shin, T., Jackson, H., Pape, D., Harrey, M.; Schuik, T., Ritter
E., Kohn, S., Shin, T., Jackson, F., Cardenas, M., McCann, R.,
Materston, R. and Wilson, R.
The Washin KI House EST Project 1999
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High quality sequence stop: 480.
Location/Qualifiers
1. 1017
/creanism-WHS musculus
/strain-C/518L.
/db.xref-'taxon:10090'
/clone-'INAGE:1887498
/clone-'INAGE:1887498
/sex-'female
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COMMENT
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Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott, J. Cain

Athersys, Inc.

3201 Carnegte Ave, Cleveland, OH 44115, USA
Fai: 216 419 9906
Fax: 216 361 9956
Fax: 216 361 9956
Fax: 216 361 9956
Fax: 216 361 9956
                                                                                                                                                 Homo saplens
Homorata Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Homomalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 791)
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88.5%; Pred, No. 3.8e-158;
tive 0; Mismatches 72; Indels 19; Gaps
              BG198890
BG198890.1 GI:13720577
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Best Local Similarity 88.57
Matches 700; Conservative
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Libraries using Random Activation of Gene Expression', Nature Bulcechnology, in press. Note that even though the Cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances.
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Creation of Genome-vide Protein Expression Libraries using Random
Activation of Gene Expression
Activation of Gene Expression
Fari Biotechnol. 19 (5), 440 (2001) In press
Contact. Scott J. Cain
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Rokaryota: Metazoa; Chordata: Craniata: Vertebrata: Euteleostomi;
Romamalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 910)
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KST1760 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence
BG198348 GI:13720035
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1180 ettetgtgetacatgacaacaaagaatteecaaccagagatgtttgacetegtest 1239 ettetgtgeterettgeset 1239 ettetgtgeterettgeset 1239 ettetgtgeterettgeset 1239 ettetgtgeterettacacettgeseker 1898 ettetgtgeterettgeseker 1898 ettetgeseker 1898 ettetgtgeseker 1898 ettetgtg
                                                                                                                                                                                            33.9%; Score 592.4; DB 11; Length 910;
87.2%; Pred. No. 7.3e-151;
Live 0; Mismatches 97; Indels 2; Gaps
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// Organism-Homo sapiens*
// Ab_Aref-'taxon;9606*
// Cone_ib-'hrhersys RAGE Library*
// Cell_line-'Hr1080*
// Cell_line-'Hr1080*
// Orde-'see 'Creation of Genome-wide Protein and Control of Genome-wide Protein and Control of Gene Ex ''---'es using Random Activation of Gene Ex ''----'es using Random Activation of Gene Ex ''----'es using Random Activation of Gene 
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Tel: 216 419 990
Fel: 216 419 990
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High quality sequence stop: 490.
High quality sequence stop: 490.
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".'sm.'Homo sapiens'
".'sm.'Homo sapiens'
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Matches 672; Conservative
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      Iligated to a Draili adaptor [IGITGGCCTACTGG], digested and choned into distinct Draili sites of the parties. Last occurred; site CACTGTTGG, 3 site CACCATGTG). Xhoi should be used to isolate the CDMA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Samio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5 and primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CCACCACGACGACACA.
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Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Manaryota; Metazoa; Chordata; Craniata: Vertebrata: Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
I (Dasea I to 907)
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Anote—"See 'Creation of Genome-wide Protein Expression
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cell type indicated is #1080, since a random activation
when was used, these sequence tags are not necessarily
expressed in #11080 under normal circumstances."
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Fig. Aurenta Metacas: Chordata: Craniata: Vertebrata; Euteleostom1: Pikaryota: Metacas: Chordata: Craniata: Vertebrata; Euteleostom1: Manmalia: Eutheria: Prinates: Catarrihini: Homindae: Homo.

Fig. 1 (bassa: 1 to 647)

Gian. B. Wu. T. Huang, C. Huang, C. Kang, B. Gao, X., Xu, Z., Xiao, H. Sois, M. Yu, Y. Liu, Y. Yu, Y. Liu, Y. Song, H., Cheng, Z., Ou, J., Zang, L. Xu, S. Ci, Y. Chen, Z. and Han, Z. Ren, S., Zhong, M., Lu C. Yu, X. Lu, C. Yu, C. Chen, Z. and Han, Z. Ren, S., Zhong, M., Lu C. Giang, Sapians chark clone

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Search completed: April 19, 2002, 08:07:44 Job time: 2764 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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April 19, 2002, 11:06:25; Search time 5830.82 Seconds (Without alignments) 1200.021 Million cell updates/sec Run on:

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IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

22023303 seqs, 10831430700 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

11: /rqn2_6/ptodata///pna/NS09_HERGED_COMB_seq1:- 27: /rqn2_6/ptodata/2/pna/NS09_HERGED_COMB_seq1:- 17: /rqn2_6/ptodata/2/pna/NS09_HERGED_COMB_seq1:- 18: /rqn2_6/ptodata/2/pna/NS09_HERGED_COMB_seq1:- 18: /rqn2_6/ptodata/2/pna/NS09_HERGED_COMB_seq1:-	red. No. is the number of results predicted by chance to have a
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	Description	92-3 Sequence 3, Appli	9 Sequence 759	9 Sequence 759,	9 Sequence 759,	Sequence 1355,		188 Sequence 188,	4 Sequence 24, 7	Sequence 9,	5 Sequence 55,	Sequence 5	Sequence 57,	Sequence 20,	Sequence 21,	Sequence 22,	Sequence 23,	Sequence 59,	Sequence 59,	Seguence 97,	Sequence 13,	Sequence 14,	10-15 Sequence 15, Appl	Sequence 16,	57 Sequence 57,	Sequence 25,	Sequence 61,	Sequence 62,	44 Seguence 744,	8-744 Sequence 7	1-744 Sequence 744,	36
SUMMARIES	a ID	30 US-09-763-292-3	55 US-60-226-176-75	56 US-60-233-468-75	-09-SD	ns-60-		_	ò	_	ns-60-		54 US-60-213-7						18 US-09-488-127B-59		_	52 US-60-494=110-1	_	ns-60-	09-SD	_	_	us.	55 US-60-226-176-7	US-60-233	US-60-313	57 IIS-60-248-4
	Query Match Length DB	323	323	323	323	572	572	572	51955	225532	10097	10097	10097	3557	3557	3557	3557	8437	8437	8437	. 685	685	685	18364	32768	99109	222537		348			4 12538
æ				3 100.0											.2 88.0												2 85.2	85	-		63 81.	E 8
	Score	32	32	32	32	310.4	310.4				299.4	299.4	299.4	284.	284.		284.2		1 276.B				23			27	27	27	1 263			26.
	Result No.		7	œ.	7	ς.	9	٥	_	ر 9	10	Ξ	17	13	=	15	16	17	18	19		c 21		23	74		ر د 5و	•	26	59	36	c 31

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TILE REPERENCE: GX-01313 Pucleotide Polymorphisms Associated With ADME Genes CURRENT APPLICATION NUMBER: US/60/233,468
CURRENT PILING DAIE: 2000-918
NUMBER OF SEQ ID NOS: 2408
SEQ ID NO 759
PERL Program
SEQ ID NO 759
Morris, MacDonald
TION: Signale Nucleotide Polymorphisms Associated With ADME Genes
Preprior: Cx-0011-1 p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         759, Application US/60233468 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: "NAME/KEY: misc_feature
: OTHER INFORMATION: GB:HUM2C9X05
US-60-233-468-759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ring, Huljun Z.
Ralsen, Gareth
Ownley, David
Forris, MacDonald
Aldes, Ana
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
CTHER INFORMATION: GB:HUM2C9X05
US-60-226-176-759
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-60-233-468-759
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Sequence 759, Application US/60226176
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-09-763-292-3
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RESULT 5
US-60-10-1355, Application US/60170373
US-60-10-1355, Application US/60170373
US-60-10-1355, Application US/60170373
US-60-10-1355, Application US/60170373
US-60-10-1355, Application US-60170373
US-60-1355, US-60-
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US-60-181-428-187/C
US-60-181-428-187.

Sequence 187. Application US/60181428

CERREAL INFORMATION

TILLE OF INVENTION: FOOLENS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES

CURREAT FILLING DATE: 2000-02-09

SOFTWARE: FREEDE DATE: 2000-02-09

SOFTWARE: FREEDE OF WINDOWS VEFSION 4.0

LENGTH: 572
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: ORGANISM: Human
US-60-170-373-1355
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95-60-313-47-759

Sequence 759, Application US/6031371

Sequence 759, Application US/6031371

SEQUENCE TROUGH TOWN

APPLICANT: NOTES ADAIGN

APPLICANT: WORLE GARCH

APPLICANT: WORLE GARCH

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APPLICANT: WORLE GARCH

TILL OF INTERTION: SINGLE NOTES BY
CURRENT PILLY OF NOTE: 2001-08-16

SUTHARE: PER FILLY OF SECUENCE CARCH

SOUTHARE: PER PROGRAM

SOUTHARE: P
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121 gcatgcaagacagggccactgcctcacacagatgctgtggtgcagaggccagagat 180
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Best Local Similarity 100.0%; Pred. No. 7.4e-9 No. 7.4e-9 No. Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; KAME/KET: misc_feature
; OTHER INPORMATION: GB:HUM2C9X0S
US-60-313-371-759
          Matches 323; Conservative
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ORGANISM: Homo sapiens
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Syequence 2.1. Aprileation US/60248498

GENERAL INFORMATION:

RPLICART: Bessley. Ellen

TILLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING

TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TILLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF

CURRENT FILLA PRICEATION NUMBER: US/60/248.498

CURRENT FILLNO DRIE: 2000-11.15

SOFTHARE: FastEDD MOS: 24

SOFTHARE: FastEDD for Windows Version 4.0

LENGTH: 51955
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216 ACTATCTCATTCCCAAGGTAAGTTGTTTCTCCTACACTGCAACTCCATTTCGAAGT
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TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TITLE OF INVENTION: DROIEINS, NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES
FILE REFERENCE: CLOO0876
CURRENT APPLICATION NUMBER: US/60/245,227
CURRENT APPLICATION NUMBER: US/60/245,227
CURRENT FILE OF DAIE: 2000-11-03
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                                                        NAME/KEY: misc_feature

// LOCATION: (1)...(51955)

OTHER INFORMATION: n = A.T.C or G

US-60-248-498-24
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US-60-245-227-9/c
Sequence 9, Application US/60245227
, ERPERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: HUMAN
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                                                                                                                                       241 actatctcattcccaaggtaagtttgttctcctacactgcaactccatgttttcgaagt 300
216 ACTACTCTTCCAAGGTAGTTGTTCTCCTACATGCAAGTCCATGTTTCGAAGT 159
216 ACTACTCTCCAAGGTAGTTGTTCTCCTACATGCAAGTCCATGTTTCGAAGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 96.1%; Score 310.4; DB 51; Length 572; Best Local Similarity 99.4%; Pred. No. 8.4-e96; Indels 1; Gaps Matches 322; Conservative 0; Mismatches 1; Indels 1; Gaps
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TITLE OF INVENTION: ISOLATED HUMAN DRUG-WETABOLIZING
TITLE OF INVENTION: ISOLATED HUMAN DRUG-WETABOLIZING
TITLE OF INVENTION: PROTEINS, NOLECLE ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
TILE REPERREE: CLOOO227
CURRENT APPLICATION NUMBER: US/60/181,428
CURRENT APPLICATION NUMBER: 100-02-09
NUMBER OF SEQ ID MOSS: 440
SCOTIANE: FESTEED for Windows Version 4.0
SEQ ID NO 188
LENGTH-51:
                                                        Score 310.4: DB 51; Length 572; Brott Local Similarity 99.44; Pred NO 8.4e-86; Indels 1; Indels 1; Histoha 32; Conservative 0; Hismatches 1; Indels 1;
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Sequence 188, Application US/60181428
GENERAL INFORMATION
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  US-50-181-428-187
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APPLICANT Bessley, Ellen
TILLE OF INVENTION: ESOLATED HUMAN PHASE I DRUG-METABOLIZING
TILLE OF INVENTION: PROCEDING, MOLLEC CALD MOLLECULES ENCODING HUMAN
TILLE OF INVENTION: PROCEDING, MOLLEC CALD MOLLECULES ENCODING HUMAN
TILLE REFERENCE: CLOGOTOS
CURRENT FILLE OF INVENTION WORDER. US/60/213,795
CURRENT FILLE DATE: 2000-06-23
NUMBER OF SED ID MOSS: 267
SED ID NO SS: 267
SED ID NO SS: 267
ENCITABLE FASISED for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                     : NAME/KEY: misc_feature
: LOCATION: (1)...(10097)
: OTHER INFORMATION: n =
US-60-213-795-56
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54378 GANGCAMAGAAGCAACATGCCTAAAAATGTGTGGTGCACGAGGTCAAAAA 54119
                                                                                                                                                                                                                                                                                                                                                                                        Ouery Watch 96.1%; Score 310.4; DB 57; Length 225532; Best Local Smilarity 99.4%; Pred. No. 11.5-94; Indels 1; Gaps Matches 322; Conservative 0; Mismatiches 11; Indels 1; Gaps
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   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9 LENGTH: 225532
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: LOCATION: (1)...(10097);
: OTHER INFORMATION: n = A,T,C or G
US-60-113-795-58
                                                                               TICRE: DAM
ORGANISM: HUMAN
PENTURE:
NAME/REI: misc_feature
LOCATION: (1) ... (222532)
G-60-100: (1) ... (222532)
G-60-125-217-9
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97.9%; Pred. No. 3.1e-77;
Live 0; Mismatches 3; Indels 4; Gaps
88.0%; Score 284.2; DB 53; Length 3557;
97.9%; Pred. No. 3.1e-77;
tive 0; Mismatches 3; Indels 4; Gaps
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TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THE
FILE REFERENCE: CLOODOSS
CURRENT APPLICATION NUMBER: US/60/207,211
CURRENT APPLICATION NUMBER: 2000-05-26
NUMBER OF SED ID NOS: 74
SOFTHARE: FASTSED for Mindows Version 4.0
SED ID NO 21
LENGTH: 355
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GENERAL INFORMATION:
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Best Local Similarity 97.9
Matches 320; Conservative
        Ouery Match 88.0°
Best Local Similarity 97.9°
Matches 320; Conservative
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: ORGANISM: HUMAN
US-60-207-211-21
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                               TILLE OF INVENTIONS: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TILLE OF INVENTIONS: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TILLE OF INVENTIONS: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUM,
TILLE OF INVENTIONS: DRUG-METABOLIZING PHASE I PROTEINS, AND USES I
FILE REPREMEE: LOBOOTOS
CURRENT ALLIATO DATE: 2000-06-23
CURRENT FILLE DATE: 2000-06-23
SOFTWARE: SESSED for Windows Version 4 P
ENDINE OF STATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Watch 92.7%; Score 299.4; DB 54: Length 10097: Best Local Similarity 99.1%; Pred. No. 9.3:282; DB Matches 312; Conservative 0; Mismatches 1; Indels 2: C
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| LOCATION: (11)...(10097)
| THER INFORMATION: n = A,T,C or G
US-60.213-795-57
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; ORGANISM: HUM
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ISOLATED HUMAN PHASE I DRUG-METABOLIZING
PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                 3: Indels 4; Gaps
                                                                                                                                                                                     88.0%; Score 284.2; DB 53; Length 3557; 97.9%; Pred. No. 3.1e-77; tive 0; Mismatches 3; Indels 4;
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100-05-26
pplication US/60207211
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Sequence 2, Application US/08201118
GENERAL HISTORMATION:
APPLICANT: GOLDSTEIN, JOYCE A.
APPLICANT: GOLDSTEIN, JOYCE A.
TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMEN
TITLE OF INVENTION: BNAS POR MULTIPLE MEMBERS OF THE HUINTIELE OF INVENTION: SUBFAMILY
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND Khourie and Crew
STREE: 379 Lytton Avenue
CORRESPONDENCE ADDRESS:
ADDRESSEE: California
COMPUTER: 18M PC Compatible
COMPUTER: 22-FEB 1994
CLASSITICATION NATA: 75-
RILING DATE: 09-ARR: 1992
FILING DATE: 09-ARR: 1992
FILING DATE: 09-ARR: 1992
NTOMBET: ARRESTEIN NATA: 77-
NAME: 11shbachurer 77-
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REGISTRATION WINBER: 17.505
REFERENCYOCKET WHEBER: 15.280-192-1
TELECOWNIN CATION I WENDRAYI ON:
TELECHONE: (415) 326-24.00
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTRESTICS:
LENGTH: 1746 base pairs
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1. cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4. cgn2_6/ptodata/2/ina/6A_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/pcrug.COMB.seq:*

6: /cgn2_6/ptodata/2/ina/packfiles1.seq:*
                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351203 seqs, 113238999 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
Sequence:
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Result No.

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1 cttcaatgatcctttgfgtccttgtgtctctgtctctcagtttgcttctcttcaa 50 	tergagemengetergagagagagaanteeteeteetegagagagagagagagagagagagagagag	tiggaaatatcitoogatagatattaaggatgicogcaaatcitaaccatcitocaa tiggaaatatcitocagatagatattaaggatgicogcaaatcittaaccatcitooa 	Anatotatggcctgtgttcactctgtattttggcttggaacgaatgtggtgctgcatg HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	9akatgagtggtgaaggaagcccgattgatcttggaagagttttctggaagagcc 111111111111111111111111111111111111	atttcccactggctgaagagctaacagagatttg 	gatgaaggagatteggegttteteceteatgaegetgeggaatttigggatggggaaa 	ggagcattgaggaccgtgttcaagaggaagccgctgcttgtggaggagttgagaaaaa 	Case Case	gciccatatiticcagaacgiticgitiiliiliiliiliiliiliiliiliiliiliidecccatatiticcagaatiticcagaacgiticgatg		661 ttoccactatcattgattatttoccgggaacccataacaaattacttaaaaaccttgctt 720 	721 ttatggaaagtgatattttggagaaagtaaaagaacaccaagaatcgatggacatcaaca 780 	781 accetcgggacttattgattgettectgateaaatggagaaggaaaagcaaac 840 	841 agtctgaattcactattgaaaacttggtaatcactgcagctgacttactt	901 cagagacaacaagcacaaccctgagatatgctctccttctcctgctgaagcacccagagg 960 111111111111111111111111111111111111	961 tcacagctaaagtccaggaagattgaacgtgtcattggcagaaaccggagccctgca 1020 	1021 tgcacgacaggggccacatgcctacacagatgtgtgtgcagaggtccagagataca 1080

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| COATION: 1.00
| COATION: 1.00
| OTHER INFORMATION: /note- Corresponds to positions .5 to-1
| GR-08-338-318-1218-2
                                       PILING DATE: 06-MAY-1994
CLASSITEATION: 435
PRIOR APPLICATION DATA: 435
PRIOR APPLICATION DATA: 435
PLING DATE: 22-FEB-1994
CLASSITEATION: 435
PRIOR APPLICATION DATA: 435
PRIOR APPLICATION HONER: 13520-192110
ATTORNET AGENT INFORMATION: 80AE: 13520-192110
TELEPOROMUTION INFORMATION: 15220-192110
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TELEPAX: (650) 336-2420
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đã	1261	<u>iaagaaagtaactacticatgectiteteageagaaaaeggattigtgtgtgggagag</u>	6
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- oy	1621	cattaaaaaagtttcactgtgcaaatatatctgctaticcccatactctataatagttac	1680

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APPLICATE TO SOLUTERN, MAIJOILE
APPLICATE TO SOLUTE H.F.
TITLE OF INVERTION: CITOCHNEE, PERSESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVERTION: CITOCHNEE PASS C219: THE PRINCIPAL DETERMINANT
TITLE OF INVERTION: CITOCHNEE PASS C219: THE PRINCIPAL DETERMINANT
TITLE OF INVERTION: CYPORESSIE: TOWNSEND AND CONTRESSEE: JOWNSEND AND CONTRESSEE: TOWNSEND AND CONTRESSEE: PASS 
  Ouery Match 99.6; Score 1739, 6; DB 5; Length 1745; Best Local Similarity 99:81; Pred. No. 0; Metches 1147; Conservative 0; Mismatches 4; Indels 0;
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PRIOR APPLICATION DATE: S07/864,962
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REPREDECTOR NUMBER: 39.684
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PLING DATE: 06-MAT-1994
PRIOR APPLICATION DATA:
APPLICATION NOMES: US 08/201,118
PLILING DATE: 22-FEB-1994
                                                                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS9505744 GENERAL INFORMATION:
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Matches 1637; Conservative
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OPERATING SYSTEM: PC-F
SOFTWARP
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APPLICANT: ROWES:
ITILE OF INVENTION:
CORRESPONDENCE ADDRESS:
SOURCES:
STREET: 379 Lytton
STREET: 379 Lytton
STRATE: California
ETT: Palo Alto
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COMPUTER READABLE FORM
MEDIUM TIPE: Floppy
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CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
MEPHENYTOIN METABOLISM
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                      APPLICANT: WOLDSAIN SUPPLY APPLICANT: WOLDSAIN SUPPLICANT: WOLDSAIN SUPPLICANT: ROMES-STARRS, MAINTED BY MONTES-STARRS, MAINTED SUPPLICANTION: CHOCKING, EXPRESSION AND DIAGNOSTILLE OF INVENTION: CTYCCHROME P450 2019; THE PRITILE OF INVENTION: WEPHENTION WETBADLISH TILLE OF INVENTION: WEPHENTION WETBADLISH CORRESPONDENCE ADDRESS: 61
CORRESPONDENCE ADDRESS: 7
STARET: TWO PUBMATCADERO CENTER, 8th Floor STRET: California
COUNTY: California
                                                                                                                                                                                                     LIP: 94111
COMPUTER READABLE FORM:
WEDINY TIPE: FLORPY disk
COMPUTER: IN PC COMPALIBLE
COMPUTER: IN PC COMPALIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PACENDE NOS/MS-DOS
CLASSIFICATION NOTA
FILING DATE: 22-FEB-1994
CLASSIFICATION AND
FILING DATE: 09-ARP-1992
FILING DATE: 09-ARP-1992
FILING DATE: 09-ARP-1992
FILING DATE: 10-PORATION:
NAME: 110-PORATION:
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LELEFAX: (650) 326-2422
INFORMATION FOR SEO IN SEQUENCE OF
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Best Local Similarity 92.99
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RESULT 5 US-08-218-8218-10 ; Sequence 10, Application US/082388218

Page 7

Oy 1321 gectggcccgcatggacttttattcctgaccttcattttaccgaactttaacctga 1380 1326 CCTGGCCGCATGACCTGTTTTATCCTGACCTCATTTACCAGACTTTAACCTGA 1385 OY 1381 aatctctgattgaccacacttctgttgtcaatggatttctg1440 1386 AATCTGGTTGACCCAAGAACTTGACACACTCCATTGCAATGGATTGCTCCTG 1445 OY 1286 CATGTCGTTGACCCAAGAACTTGACACACTCCAGTTGTCAATGGATTGCTCTG 1445 OY 1446 TGCCGCCTTGTTACCAGCTGCTTCATTGCTGAAGAACGAAGACCAGTGCCTGCTG 1505 OY 1501 CCCGCTTGACCAGCTGCTTCATTCCTGTCGAAGAAGACAGAC		PESULT 6 PCT-1929-105744-10 SEQUENCE 10, APPLICATION PC/TUS9505744 SEQUENCE 10, APPLICATION PC/TUS9505744 SEQUENCE 11 FORMES SPARKS, Marjorie APPLICANT: GOLJOSTEIN, JOyce A. APPLICANT: DE NORES SPARKS, Marjorie APPLICANT: DE NORES SPARKS, Marjorie TITLE OF INVENTION: CTTCCHROWE P450 2019: THE PRINCIPAL DETERMINANT TITLE OF INVENTION: CTTCCHROWE P450 2019: THE PRINCIPAL DETERMINANT TITLE OF INVENTION: CTTCCHROWE P450 2019: THE PRINCIPAL DETERMINANT TITLE OF INVENTION: CTTCCHROWE P450 2019: THE PRINCIPAL DETERMINANT CORPRESONMENTE AND PROPERTY OF THE PRINCIPAL DETERMINANT CORPRESONMENTE AND PROPERTY OF THE PARABOLISM CORPRESONMENTE AND PROPERTY OF THE PARABOLISM	MDDRESSE: Townsend and Townsend Khourie and Crew STREET: 179 Lytton Avenue CITY: Palo Ale Callornia CITY: Palo Ale Callornia COUNTRY: 015 CONFOURR READABLE FORM: COMPUTER READABLE FORM: COMPUTER 194 COMPUTER: 194 PC COMPATIBLE CONFOURRER: 194 PC COMPATIBLE COMPUTER: 194 PC COMPATIBLE CONFOURRER: 194 PC COMPATIBLE CONFOURRER: Patentin Release #1.0, Version #1.25	CURRENT APPLICATION DATA: CURSTING DATE: CLASSIFICATION WHER: PCT/US95/05744 FILING DATE: CLASSIFICATION NUMBER: WG 08/238.821 FILING DATE: 06-MAY-1994 PRIOR APPLICATION NUMBER: US 08/201.118 FILING DATE: US 07/864.962 FILING DATE: US 07/864.962
241 gatatgaagtggtgaaggaagccctgattgatcttggagagggttttctggaagaggcc 300 246 GATATCAACCAACCAACCAATGACTTGGAAGAGACTTTTTTGAAGAGACACA 305 301 atttcccactggctgaaagagctaacagaggatttggaatcgtttcagcaatggaaga 300 atttcccactggctgaaagagctaacagaggatttggaatcgtttcagcaatggaaaga 300 atttcccactggctgaaagagctaacagaggatttggaatcgtttcagcaatggaaaga 300 atttcccactggctgaaagagctaacagagatttggaatttggaaaga 300 atttcccactggctgaaagagctaacagagatttggaattggaaaga 301 attgaaagaagttcagcctaAcAaGaGATTGAATTGTTCAACAATGAAAA 302 attgaaagaagttcagcgttctcccccactagagagctggaattttgggaaga 420 attgaaagaagttcagcggttctccccccactttgggagaattttgggaaga 421 gaagaaagagttcagcggttcacccccactttgggagaaga 422 attgaaagaagttgaaagaagaagaagaagaagaccggttgtggagaaga 423 attgaaagaagttgaaagaagaagaagaagaccggtgtgtggagaaga 424 attgaaagaagaagaagaagaagaagaagaccggctgtgtgggagaagaaga 425 attgaaagaagaagaagaagaagaagaagaagaagaagaa	541 garcocattattatcosasascgttogstatassaspatcocasattattastags 600	721 ttatggaaagtgatattttggagaaagtaaaagaacaccaagaatcgatggacatcaaca 780	901 cagagacaacaagcacaaccctgagatatgctcccttcctqctqaaqcacccaagg 960 906 CAGAGACAAACACAAACCCTGAGATATGCTTCTTCTTCTTCTTCTTCTTTTTTTT	1081 tegactcatcccaccagcctgcccatgcagtgacctgtgacgtcaattcagaaact 1140

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LENGTH: 1852 base
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APPLICANT: GOLDSTEIN, JOYCE A.
APPLICANT: ROKKES-SPARKS, MATJOTIE
TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
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US-08-201-118-4
Sequence 4, Application US/08201118
: Patent No. 5786191
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TITILE OF INVENTION: DNAS FOR MULTIPLE HEMBERS OF THE HUMAN CYTOCHROME P450 20 TITLE OF INVENTION: SUBFAMILY
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CORRESPONDENCES: 45
CONTINE Palo Alto
COUNTRY: 05
COUNTRY: 05
COMPUTER: 104 PC Compatible
COMPUTER: 105 PC COSTANTON
COMPUTER: 105 PC COSTANTON
COMPUTER: 105 PC COSTANTON
COMPUTER: 20 PC PC 105 PC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE T
US-08-201-118-4
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g	428 GGAGCATTGAGGACCGT	GITCAAGAGGAAGCCGGCTGCCTTGTGGAGGAGGTTGAGAAAA 487	
λó	1 ccaaggetteacetg	jateceaettteateetgggetgtgeteeetgeaatgtgatet 5	0
Q _Q	488 CCAAGGCCICACCCIGIO	SATCCCACITICATCCTGGGCTGTGCTCCCTGCAATGTGATCT 54	7
oy.	541 getecattattttecag	apacgtttcgattataaagatcacgaattcttaacttgatgg 60	0
q O	8 GCTCCATTATTTCCAT	AAACGITIIGAITATAAAGAICAGCAATTTCTTAACTTAA	7
0,	l aaaaattgaatgaaaa	œ.	
QQ	8 AAAGTTGAATGAAA	rcaagattttgagcagccctggatccagatctgcaataatt 66	7
ζò	1 ttece	tatttcccgggaacccataacaattacttaaaaaccttgctt 7	0
qa	8 TITCICCIAICATIGA	TACTICCCGGGAACTCACAAAATAACTTAAAAAACGTTGCTT 72	
oy	721 ttatggaaagtgatatt	ttggagaaagtaaaagaacaccaagaatcgatggacatcaaca 78	0
đ	B TIATGAAAGTIATAT	TTGGAAAAGTAAAAGAACACCAAGAATCAATGGACATGAACA 78	7
0y	781 acctcgggactttatt	gattgetteetgateaaaatggagaaggaaageaaagea	0
qq	8 ACCTCAGGACTITAL	SATIGCTICCTGAIGAAATGGAGAAGGAAAGCACAACCAAC 84	7
Oy	841 agtctgaattcactatt	gaaaacttggtaatcactgcagctgacttacttggagctggga 9	0
qG	8 CATCTGAATTTACTAT	saaagciiggaaaacacigcagiigaciigiitggagciggga 90	7
oy	agagacaacaagcac	tatgeteteetteteetgetgaageaceegagg 96	Q
qq	B CAGAGACGACAAGCAC	CCTGAGATATGCTCTCTTCTCTGTGAAGCACCAGAG	7
9.y	cacagetaaagteca	gaagagattgaacgtgtcattggcagaaaccggagcccctgca 102	~
qq	68 TCACAGCTAAAGTCCA	GTGATTGGCAGAAACCGGAGCCCCTGCA 102	72
oy	cacgacaggggcca	108	æ
qq	9 TGCAAGACAGGAGCCA	Argeceracacaraciereresecacaagarecagagarace 108	m
oy	81 tegaceteateceeac	cagectgececatgeagtgaectgtgaegttaaatteagaaact 1140	0.
QQ	88 IIGACCIICICCCCAC	AGCCIGCCCAIGCAGIGACCIGIGACATIAAATICAGAAACT 114	-
δò	1141 acctcattcccaagggg	cttcctcacttctgtgctacatgacaaca 120	Ó
QQ	48 AICTCATTCCCAAGGG	ACAACCATATTAATTTCCCTGACTTCTGTGCTACATGACAACA 120	0
0,	tttcccaacco	ctcgtcactttctggatgaaggtggaaatt 126	ω.
Q _C	08 AAGAATTICCCAACCC	SAGATGITIGACCCICATCACTITCIGGATGAAGGTGGCAATT 126	•
9		ttcatgcctttctcagcaggaaaacggatttgtgtgtgggagagg 132	~
qq	68 TTAAGAAAAGTAAATA	CTTTCTCAGCAGGAAACGGATTTGTGTGGGGGAGAG 132	327
03	ctggcccgcatgga	ctgtttttattcctgaccttcattttacagaactttaacctga 138	œ.
ପୁଘ	1328 CCCTGGCCGGCATGGAC	TITIAITCCTGACCTCCATTTTACAGAACTTTAACCTGA 138	181
0.7	tetgattgacce	naaggacettgacacaacteetgttgteaatggatttgettetg 144	140
qo	88 AATCTCTGGTTGACCC	AAGAACCIIGACACCACICCAGIIGICAAIGGIIIIGCCICIG 144	4
0,	41 tecegeeettetatea	gretteatteetgtetgaagaageacagatggtetggetg 150	Ò
qq	48 IGCCCCCTICIACCA	CIGIGCITCATICCTGTCTGAAGAAGAGCAGATGGCCTGGCTG 150	Ö
97	1 ctcctgtgctgtccct	getetettteetetggtecaaattleactatetg 155	Δ.
đ	1508 crecrerecastecer	caderererricereresescarrarecarerreceraters 156	267

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961 teacagetaaagtecaggaagattgaacgtgteattggcagaaaceggageeetgea 1020
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                                                                                                                                                                                                                                                                                                                                                           661 ttcccactatcattgattatttcccgggaacccataacaaattacttaaaaaccttgctt 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841 agtotgaattoactattgaaaacttggtaatoactgcagctgacttacttggagctggga 900
                                                                                                                                                                                                          301 attteceaetggetgaaagagetaacagaggatttggaategtttteageaatggaaaga 360
                                                                                                                                                                                                                                                                                                                               601 aaaaattgaatgaaacatcaqgattgtaagcacccctggatccagatatgcaataatt 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 87.6; Score 1529,8; DB 2; Length 1854; Best Local Similarity 92.7%; Pred. No. 0; Marches 154; Conservative 0; Mismatches 112; Indels 17;
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                                                                                                                                                                                                                                                                                                                  EXPRESSION AND DIAGNOSIS OF HUMAN IE P450 2C19: THE PRINCIPAL DETERMINANT OF S-
1554 tyatgettettetgacegicalcteacatttecettececeagalctagigaacatt 1513
1564 TATACCTIFECTACTGETTACTACTGACTGAACTTTTCCTIFCCTGAACATTACTAGIGAACATT 1527
                                               /note= "Corresponds to positions -12 to-1 for 25 of Figure 2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LIP STREET: Two Embarcedero Center, 8th Floor STATE: San Francisco STATE: California COUTH:: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER: US/08/238,821B
: 06-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ER: US 07/864,962
                                                                                                                                                                                                                                       Sequence 4, Application US/08238821B
Patent No. 5912120
GENERAL INFORMATION:
                                                                                                                                                  FILING MALE
ATTORIET/AGERT INFORMATION:
MANE: Liebeschuetz, Joe
REGISTRATION HUNGER: 37 -
REGISTRATION HUNGER: 37 -
REGISTRATION HUNGER: 37 -
REGISTRATION HUNGER: 37 -
TELECOMMUNICATION 1326-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy di:
COMPUTER: IBH PC compat
OPERATING SYSTEM: PC-DO
                                                                                                                                                                                                                                                                                          APPLICANT: ROMRES-SPARK,
APPLICANT: DE MORALS, SC
TITLE OF INVENTION: CLON
TITLE OF INVENTION: CTO
TITLE OF INVENTION: MEPI
UNDERS OF SEQUENCES: 61
CORRESPONDENCE ADDRESS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111
MPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
-08-238-8218-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION
APPLICATION NUM
FILING DATE: 06
CLASSIPICATION:
PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATURE:
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us-09-763-292-1.rni

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MEDIUM TIPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
CORPLIAN: TBM PC COMPATIBLE
COFTARE: PETCHIN Release #1.0, Version #1.25
SOFTARE: PETCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05744
FILING DATE: CLASSIFICATION NUMBER: US 08/238,821
FLINS DATE: 06-MAY-1994
FRIOR APPLICATION NUMBER: US 08/238,821
FRIOR APPLICATION NAMPER: US 08/201,118
                                                                                                                                                                                                                                                                                     09-APR-1992
                                                                                                                                                                                                                                                   BER: US 08/201,118
2-FEB-1994
                                                                                                                                                                                                                                                                    FILING NATE, 22-FEB-1994
PRIOR APPLICATION DATA. B.
FILING DATE: 99 APR-1992
ATTORNET AGENT INFORMATION:
NAME: DOV. READ B.
REGISTRATION NOMBER: 29.69
                      1141 accteatreceasggeacaacatattaactteecteacttetgtgetacatgacaaca 1200
                                                                                                                                                                                                                                                                          1201 aagaatteccaacccaagagatgtEtgaccctcgtcactteCtgatgaaggtggaaatt 1260
1208 AAGATTCCCAACCCAAGATGTTGACCTCATGATTTCTGATGAAGTGGGAATT 1267
                                                                                                                                                                                                                                   1148 APCPCATTCCCAAGGGCACAACCATATTAATTTCCCTGACTTCTGTGCTACATGACAACA 1207
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REGISTRATION NUMBER: 29,6
REPREMEMEDOCACHT NUMBER:
TELECOMONICATION TROOMATI
TELETONER: (415) 356-3407
TELETAX: (415) 66-3407
TELETAX: (415) 66-3407
SEQUENCE: CHARACTERISTICS: STRANDEDNESS: TOPOLOGY: li . MOLECULE IY PCT-US95-05744-4 ò g ò 6 õ a 1441 tcccgccttctatcagctgtgcttcattcctgtctgaagaagcacagatggtctggctg 1500 1448 receccerreraceaecrerecretrearrecrerereaaaaaaacaargeceregere 1507 1664 tactotataatagitacatigagigocacataaigoigatactigictaaigitgagita 1723 1588 IACTCIGIAACAGIIGCAIIGACIGICACAIAAIGCICAIACIIAICIAAIGIIGAGIIA 1747 合 8 8 윱 8 g Š g Š 윱 5 g ç 윰 5 윰 δ

ROMKES-SPARKS, Marjorie
DE MORIS, SOLIA M.F.
VERTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
VERTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
VERTION: CTCCHROME P450 2C19: THE PRINCIPAL DETERMINANT
VERTION: OF S-MEPHYNTOIN METABOLISM
DEQURECES: 61 Sequence 4, Application PC/TUS9505744 GENERAL INFORMATION: APPLICANT: DE HORA TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES RESULT 9 PCT-US95-05744-4

Townsend and Townsend Khourie and Crew ZIP: 94301 COMPUTER READABLE FORM California STREET: 375 C. CITY: Palo Alto CITY: Palo Alto STATE: Callfor COUNTRY: US TO BE A 4101 CORRESPONDENC ADDRESSEE:

5; 421 goagaattgaggaccgtgtcaagaggaagccccgctgccttgtgagagaattgggaaaa 480 428 GGACATTGATTTTTAARAGGAGCCCGTTGTGAGGAGATTAAAAA 487 121 tiggaaatatectacagatagatattaaggatgicageaaateettaaceaateteteaa 180 Ouery Match
B97.6%; Score 1529.8; DB 5; Length 1854;
Best Local Similarity 92.7%; Pred. No. 0;
Mstches 1534; Conservative 0; Mismatches 112; Indels 17; Gaps q ò Q ò g ò

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THERE OF INVESTIGNT SOURCE A.

APPLICANT: ROWERS SPARS, Wall of A.

APPLICANT: ROWERS SPARS, Wall of A.

TITLE OF INVESTION: CLOUNER AND EXPRESSION OF COMPLEMENTARY

TITLE OF INVESTION: DNAS FOR MULTIPLE NEMBERS OF THE HUMAN CYTOCHROME P450 2C.

TITLE OF INVESTION: SUBSEMBLY

THOMERS OF SEQUENCES: 44

CORRESPONDENCES: 44

CORRESPONDENCE ANDRESSE: TOWNS and TOWNS and TOWNS and Crew

STREET: 379 Lytton Avenue

STATE: California

COUNTRY: US

COUNTRY: US
                                                                                                                                1664 Lactetalaatagttacattgagtgecacataatgetgatacttgtetaatgttgagtta 1723
| 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1711 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 | 1747 |
Ouery Match 82.3%: Score 1436.4: DB 1; Length 1892; Best Local Similarity 86.5%; Pred: No. 0; Mismatches 1253; Conservative 0; Mismatches 221; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOP: 49.300
COMUTER READABLE FORM: 184
WEDUN TIPE: FLORPY disk
COMUTER: 184 FC COMPALIBLE
COMPUTER: 184 FC COMPALIBLE
SOFTMARE: PETENT RECEASE 11.0, VC
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPELICATION NUMBER: US/08/201.118
FILME DATE: 2-FEB 1994
FILME APPLICATION: 43
RAPLICATION DATE: 45
FILLICATION NUMBER: US 07/864,962
FILLICATION NUMBER: US 07/864,962
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                RESULT 18-14
US-08-201-118-14
Sequence 14, Application US/08201118
FPLENT NO 5786101
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,50
REFERENCE/DOCKET NUMBER: 1
:LECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1892 base pair
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121 ttggaateaccaaccapteacattaaggatgcagcaatccttaaccaatctccaa 180 	181 aaatctatggcctgtgttcactctgtatttggcctggaacgcatggtggtgctgcatg 240 11	galatgaagtugttaaggaagcccgaltgalcttgaagagagtttcttgaagaagcc Galatgalataagaagcccagaltgaltaatcattgaagagtatttcttgaagaagcc Galatgalataatcaatcaagcccaagcccaacaacaacaacaacaacaacaacaac	atticcactgotgaaagactaacagagattggaatcgtttcagcaatggaaaga TIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	gatgaaagagattcggcgtttctccccaagacgcgcgcgaattttgggatggaaga familalinininininininininininininininininin	ggagcattgaggaccgtgtcaagaggaagcccgctgctgtggaggagttgagaaaa 	caaagctcaccctggatccacttcacccgggctggctcccgcaatggcc	atcacgaattettaacttgatgg	aaaaattgaalgaaaacatcaggattgtaagcacccctggatccagatatgcaatatt 	teccentates at the technique of the tech	721 ttatggaaagtgatattttggagaaagtaaaagaacaccaagaatcgatgacatcaaca 780 	781 acctcgggactttattgattgcttcctgatcaaatggagaaggaaagcaac 840 	841 agtctgaattcactattgaaacttggtaatcactgcagctgacttactt	901 cagagacaacaagcacaacctgagatatgutctccttctcctgctgaagcaccagagg 560	961 tcacagctaaagtccaggaagaattgaacgtgtcattggcagaaaccggagccctgca 1020 	1021 tgcacgacagggccacatgcctacacagatgctgtggtgcacgaggtccagagataca 1080 	1081 togaceteatececaceagoctgceceatggagtgacetggacgttaaateagaaact 1140 1118 till	1141 accteatteceasggcaeascatattaactteceteattggtgctacatgacaaca 1200 1178 ACTEATRECEASGGCAACCATATAACHTCCTGACTGTGTGCTACATGANACA 1237	1201 aagaatttoccaacccagagatgtttgaccctcgtcactttctggatgaaggtggaaat 1250

Page 14

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961 tcacagetaaagteeaggaagaattgaaegtgteettggeagaaaeeggageeetgea 1020

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218 AASTCATGCCTGTGTCACTATTTTGGCTGAAACCCATGGTGTGGTGTGTG 277
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                                                                                                                                                                                                                                                                                                                               NAME/EXE: Region
LCALTON: 11.41
COTHER INFORMATION: /note= "Corresponds to positions -41 to-1
GTHER INFORMATION: for 2c of Figure 2."
                                                         280-192110US
                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                  TELEPHONE: (650) 326-24
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LEWITH: 1892 base pa;
                         TORNET/AGENT INFO
NAME: Liebeschue
REGISTRATION NUMB
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Pred. No. 0;
0; Mismatches 221; Indels 17; Gaps
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CITT: Palo Alto
STATE: Californa
COMPAT: Californa
COMPOTER READABLE FORM:
REZION TIPE: Floppy disk
COMPOTER: TBM FC compatible
FILING TAME: PATENTING TAME
FILING TAME: FC TAMES 
                                                                                                                                                                                                                                                            COURTE OF INVESTIGNE CADRING, EXPRESSION AND DIAGNOSS TITLE OF INVESTIGNS CYTOCHROME PASO 2019. THE PRINCIPLE OF INVESTIGNS OF S-WEPHINTION METABOLLSM CORRESPONDANCE ADDRESS:

CORRESPONDANCE ADDRESS:

STREET: 179 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09 APR-1992
ATTORNEY/AGERT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUBER: US 08/238,821
FILING DATE: 06-MAY-1994
PRIOR APPLICATION NATA: US 08/201,118
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-PEB-1994
                                                                                                                                 Sequence 14, Application PC/TUS9505744 GENERAL INFORMATION:
1778 TTGNNANNTNTTAINANN 1800
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Best Local Similarity 86.5%;
Matches 1525; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dow, Karen B. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER: TELECOMOUNICATION INFORMATION (415) 326-340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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FOR SEC
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EDUENCE CHARACT
LENGTH: 1892
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Ouery Match 78.7%: Score 1373.6; DB 2; Length 1591; Best Local Similarity 93.4%; Prefet No. 0; Mismatches 9; Indels 3; Matches 1446; Conservative 0; Mismatches 99; Indels 3;

: ANTI-SENSE US-08-194-981E-

1724 ttaacatattattattaaataga 1746

1778 TTGNNANNTNTTATNANTNANA 1800

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MEDIUM TIPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NAME: US/08/194, 981E
FILING DATE: Pebruary 10, 1994
CLASSIFICATION: 435 HUMAN CYTOCHROME P450 TITLE OF INVENTION: EXPRESSION AND TITLE OF INVENTION: BURNA TITLE OF INVENTION: BURNA TITLE OF INVENTION: CITCHROME P455 CORRESPONDERS: 68 CORRESPONDERS: ADDRESSEE: NEEDLE & ROSENBERG, P. STREET: SILLE 1200, 127 PEACHINE CITY: ALABIA STATE: GOOGRAPHE USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: RADABLE FORM: WENDING TIPE: PIOPPY 415K Sequence 3, Application US/08194981E Patent No. 5886157 GUENGERICH, F. Peter GUO, Zuyu NFORMATION:

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546 attatiticcaqaaacgilicgaltataaacalcacgaatilicitaactigaiggaaaa 605
541 ATMITICATAACGIIIGATATAAAGAICAGCAATICITAAAG 600
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848 iGANIGANACATCAGATTTGAGCAGCCCIGAATCAAATTTTTCC 607
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February 10, 1994
                      FILING DATE: February 10, 11-CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ELIZabeth Selby:
REGISTAATION NUMBER: 38,298
REGISTAATION NUMBER: 22,298
RECISTAATION NUMBER: 22,298
TELECOMMUNICATION INFORMATION:
TELEFRAX: (404) 688-0770
TENCHALI
                                                                                                                                                               : TOPOLOGY: linear
HOLECULE TYPE: DNA
HYPOTHETICAL: NO
SANTI-SENSE: NO
US-08-194-981E-4
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1021 GACAGACACACACACACAGTGTGTGTGACAGGGTCACAGATGCATTGL 1080
GEREAL INFORMATION:
APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUENGERICH, F. DEL
APPLICANT: GUENGERICH, F. DEL
TITLE OF INVENTION: RUNAN
TITLE OF INVENTION: GUENGERICH PISO
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: NEEDLE & ROSENBERC, P.C.
STREET: SLILE 1200, 127 Peachtree Street, NE
CITT. Atlanta
STATE: Georgia
COMPTRE: Guengerich Georgia
COMPTRE: Guengerich Georgia
MEDIUM TITUE: Ploppy disk
COMPTRE: The Comparation COMPTRE: The COMPTRE: The COMPTRE: The COMPTRE: The COMPTRE: The COMPTRE: The COMPTRE: PC-DOS/MS-DOS
SOPTHANE: Patentin Release 41.0, Version 41.25
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02-08-194-981E-4
15-6quence 4. Application US/08194981E
15 Patent No. 5886157
16 GENERAL INFORMATION:
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Ouery Match 73.1%: Score 1276; DB 2; Length 1419; Best Locad Similarity 94.0%; Pred. Mo. 0; Best Locad Similarity Opt.00 0; Mismatches 85; Indels 0; Gaps Matches 1371; Conservative 0; Mismatches 85; Indels 0; Gaps
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Patentin Release #1.0, Version #1.25
CATION DATA:
                                                                                    APPLICATION NUMBER: US/US/US/US. IB FILING DAIE: 22-FEB-1994
CLASSITGATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
ATOMEVACENT INFORMATION:
NAME: Liebeschuetz, Joe
REDISTATION UMBER: 15.50-192-1
IELECHONE: (415) 326-240
IFLEROWEICTION INFORMATION:
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: MOLECULE TYPE:
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DAURES-SPARRS, MAIOLICE, MAIOLICE CONPLEMENTARY
WITON: CLONING AND EXPRESSION OF CONPLEMENTARY
WITON: DNAS FOR MULTIPLE HENBERS OF THE HUMAN CYTCCHROME P450
THORS: SUBFAMILY
THORS: SUBFAMILY
TREES: 44
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Sequence 6, Application US/08201118
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APPLICANT: COLDSTEIN JOY
APPLICANT: COLDSTEIN JOY
APPLICANT: ROMES SPRAKS,
TITLE OF INVENTION: CLONIN
TITLE OF INVENTION: SUBSAN
TITLE OF INVENTION: SUBSAN
THIRD OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEN TOWNSEN AND
STREET: TOWNSEN AND
STREET: California
CONTRIET: 4101

LIP: 94101

LIP: 94101

COMPUTER: TORP COMPATINE
COMPATINE STSTEM: PC-TOOS/
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Ouery Match 72.4%: Score 1264 6; DB 1; Length 2009; Best Local Similarity 84.4%; Pred. No. 0; Matches 1489; Conservative 0; Mismatches 254; Indels 22; Gaps
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L16878 Homo sapien

Description

DB

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Sequence:	743 1 tcagaaatatttgaagcctgttagctcatgtgaagcgggg 743	311	254.6	35.6	463	
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		KEYWORDS		P2C9; C	CYP2C9; cytochrome	ě
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BC0279
AR071581
AR071581
AR071581

0775

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

Cloning and expression of complementary DNAs for multiple members of the human cytochrome P450IIC subfamily blochemistry 30, 3247-3255 (1991) 5118740 2 (bases 1 to 743) sapiens yota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi: lia; Eutheria; Primates; Catarrhini; Hominidae; Homo. XX02 743 bp DNA PRI 08-FEB-1999 sapiens cytochrome P4502C9 (CYP2C9) gene, exons 2 and 3. .ein, J.A., Raucy, J.L., Blaisdell, J.A., Faletto, M.B. and 8.1 GI:291608 9: cytochrome P450; mephenytoin 4-hydroxylase. ALIGNMENTS Romkes, M. JOURNAL MEDLINE REFERENCE TITLE

E10639 Human cDNA E10862 cDNA encodi

E14930 E10866 E10866 E10866 E10865 HUMCYPC219 HUMSVP450A ARO4195 E10095 E10095 HUMCYPC18 ARO71577 ARO71577 ARO71580 HUMCCYPC18 E10639 E10639

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Center code: SC
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KEYWORDS
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de Morais,S.M., Schweikl,H., Blaisdell,J. and Goldstein,J.A.
Gene structure and upstream regulatory regions of human CYP2C9 and
CYP2C18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Romkes,M., Faletto,M.B., Blaisdell,J.A., Raucy,J.L. and
Goldstein,J.A.
Correction: Cloning and expression of complementary cDNAs for
multiple members of the human cytochrome P450IIC subfamily
Biochemistry 32, 1390-1390 (1993)
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                     Biochem. Biophys. Res. Commun. 194 (1), 194-201 (1993)
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Pred. No. 1.1e-197;
0; Mismatches 2;
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1. .743
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Local Similarity 99.7%;
No. 741; Conservative (
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Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 143087)
Johnson, C.
Johnson, C.
Johnson, C.
Johnson, C.
Submitted (26-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14529836.
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Determinator Big Dye; 100% of reads
Consensus quality: 14266 bases at least 040
Consensus quality: 142843 bases at least 030
Consensus quality: 142843 bases at least 030
Insert size: 142987; sum-of-contigs
Insert size: 156404; aganose-fp
Ouality coverage: 8.55x in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                      gagaaaaaccaagggtgggtgaccctactccatatcactgaccttactggactactatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL359672.17 G1:14575223
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Primates;
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DD 150754 ICAGAAATATTIGAAGCCTGTGTGGCTGAATAAAAGCATACAAATACAATGAAAATATCA 150813
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                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 173136 bases at least 040
Consensus quality: 173136 bases at least 030
Consensus quality: 173145 bases at least 020
Insert size: 173154; sum-of-contigs
Insert size: 116005; 33.1% error; agarose-fp
Contage: 6.48x in 020 bases; sum-of-contigs Quality
coverage: 9.80x in 020 bases; agarose-fp
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AL133513.11 G1:14575067
HTG: HTGS_PHASE2: HTGS_ACTIVEFIN: HTGS_DRAFT; HTGS_FULLTOP
human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a "working draft" sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available if the accession number will be preserved.

1. Occation/Qualifiers
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 173154)
Brown J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 728.8; DB 2;
Pred. No. 1.5e-194;
0; Mismatches 2;
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/chromosome="10"
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/clone_lib="RPCI-11.2"
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*** SEQUENCING IN
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                                                                                                                                             Score 728.8; DB 2;
Pred. No. 1.5e-194;
); Mismatches 2;
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47106. 143087
/note="assembly_fragment:00967"
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                         /note="assembly_fragment:00494 clone_end:SP6
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Best Local Similarity . 99.6%;
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                                              AGAGCICCICGGGCAGAGCIIGGCCCAICCACAIGGCIGCCCAGIGICAGCIICCICITI 151173
150994 GTITICIGGAAGAGGCATITICCCACIGGCIGAAAGAGCIAACAAGAGGATITGGIAGGIG 151053
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Mashreghi Wohammadi,M.

Direct Submisson.

Submitted (11-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery%sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On Jun 14, 2001 this sequence version replaced gi:14148873.
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SEQUENCING
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                                                                                          ALS83836.11 GI:14455940
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLIOP
                                tgcatgtgcctgtttcagcatctgtcttggggatggggaggatggaaaacagagacttac
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Catarrhini; Hominidae;
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Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Primates;
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• NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. But the exact sizes of the gaps are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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93.5%; Pred. No. 2.8e-168;
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1. 205791
1. 205791
Adb_xref="taxon:9606"
Adb_xref="taxon:9606"
Achromosome="lo"
Aclone="RP11-466J4"
Aclone="RP11-466J4"
Anote="assembly_fragment:00191
fragment_chain:1"
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Anote="assembly_fragment:01703
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                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
27-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14529836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGRP4; version 4.5 Sequencing vector: TARP4; version 4.5 Sequencing vector: Plasmid; L08752; 100% of reads Sequencing vector: Plasmid; L08752; 100% of reads Consensus quality: 14266 bases at least 0.4 Consensus quality: 142843 bases at least 0.30 Consensus quality: 142920 bases at least 0.30 Insert size: 142987; sum-of-contigs Insert size: 156404; agarose-fp Coulity coverage: 8.55% in 0.20 bases; sum-of-contigs Quality coverage: 7.82% in 0.20 bases; agarose-fp
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Catarrhini; Hominidae;
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PROGRESS ***, 2 unordered pieces.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
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42275 ICIICACIAGIGACGICCTIGGAAACATITCAGGGGGGGGGCCAGGICTTCATIGCGCAICC 42215
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                                                                                                                                                                                                                                                                                   42873 AGTCTGAATCATACATAGTATTTGGAGCAAATAGCGACTTATTTTGCTGCTATTTGCATT 42814
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HIG: HIGS_PHASE2: HIGS_ACTIVEFIN; HIGS_DRAFT; HIGS_FULLTOP
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RP11-361K9,
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Pred. No. 2.5e-111;
0; Mismatches 164;
vector_side:left"
47106. 143087
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a 26155 c 27788 g 47797 t
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PROGRESS ***, in ordered pieces.
AL157835
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Local Similarity 77.3%;
les 577; Conservative
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                Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                               Direct Submission
Submitted (05-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 8, 2001 this sequence version replaced gi:14586042.
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                                                                                                                                                                                                                                                                                        Assembly program: XGA44; version 4.5
Sequencing vector: plasmid, L08752; 100% of reads
Sequencing vector: plasmid, L08752; 100% of reads
Consensus quality: 156104 bases at least 040
Consensus quality: 156214 bases at least 030
Consensus quality: 156246 bases at least 030
Insert size: 156492; sum-of-contigs
Insert size: 156975; 13.7% error; agarose-fp
Quality coverage: 8.34x in 020 bases; sum-of-contigs Quality
coverage: 9.69x in 020 bases; sum-of-contigs Quality
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
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46.6%; Score 346.4; DB 2;
Best Local Similarity 78.1%; Pred. No. 9.7e-87;
Matches 478; Conservative 0; Mismatches 105;
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1. .156492
/note="assembly_fragment:03685
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Web site: http://www.sanger.ac.uk
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/db_xref="taxon:9606"
Homo sapiens
Eukaryota: Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/clone="RP11-361K9"
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Blakey, S.
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                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DB 103986 ACIGGGCAGIGGCIAIAGGGAIGGGGAGGAIGGAAAAC--AGGCIIGAAGAGCICCIGGG 104043
                                                  Homo sapiens (library: EMBL3 library from J. A. Goldstein) liver
                                                                                                                                                                                                                                                                                                                                                                                                                                    HUM2C18X02 654 bp DNA PRI 24-AUG-1993 Homo sapiens cytochrome P4502C18 (CYP2C18) gene, exons 2 and 3. L16870.1 G1:291600 CYP2C18; cytochrome P450; mephenytoin 4-hydroxylase.
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2 (bases 1 to 654)
de Morais,S.M., Schweikl,H., Blaisdell,J. and Goldstein,J.A.
Gene structure and upstream regulatory regions of human CYP2C9
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Goldstein,J.A., Raucy,J.L., Blaisdell,J.A., Faletto,M.B.
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3,<1. .51)
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Biochem. Biophys. Res. Commun. 194 (1), 194-201 (1993)
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/tissue_type="liver"
/tissue_lib="EMBL3 library from J.
order(Li6869.1:1438. .>1668.<1. .5
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52. .214
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/citation=[3]
/number=2
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requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14456168.
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                                                                                     Center project name: bA400G3
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Matches 516; Conservative
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Homo.
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Direct Submission
Submitted (03-JUL-2001) Sanger Centre, Hinxton, Carbridgeshire,
CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 ggggatggggatggaaaacagagacttacagagctcctcgggcagagcttggccat 388
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*** SEQUENCING I
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HIG; HIGS_PHASE2; HIGS_ACTIVEFIN; HIGS_DRAFT; HIGS_FULLIOP
                                                                                                                                                                44.6%; Score 331.2; DB 9; Length 554:
80.8%; Pred. No. 1.8e-82;
Live 0; Mismatches 78; Indels 25
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Catarrhini; Hominidae:
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                                                                                                                       212
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407. 556
/gene=CYP2C18*
/citation=[1]
/citation=[3]
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Mammalia; Eutheria; Primates;
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            215. .406
/gene="CYP2C18"
/number=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                  Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Sequencing vector: plasmid; L08752; 100% of reads Consensus quality: 172989 bases at least Q40 consensus quality: 173136 bases at least Q30 consensus quality: 173145 bases at least Q30 lnsert size: 173154; sum-of-contigs flast Q20 lnsert size: 160005; 33.1% error; agarose-fp coverage: 6.48x in Q20 bases; sum-of-contigs Quality coverage: 6.48x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      • NOTE: This is a 'working draft' sequence.
• This sequence will be replaced
• by the finished sequence as soon as it is available and
• the accession number will be preserved.

Location/Qualifiers
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Pred. No. 5.5e-81;
0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/clone="RP11-4003"
/clone="lb="RPCI-11.2"
1. 173154
/note="assembly_fragment:00748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58012
                                Contact: humquery@sanger.ac.uk
Center code: SC
Web site: http://www.sanger.ac.uk
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7 :

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DEFINITION
ACCESSION
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ORIGIN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                              clone RP11-466J14, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (11-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 14, 2001 this sequence version replaced gi:14148873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XARAP4; version 4.5
Assembly program: XARAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Sequencing vector: plasmid; L08752; 100% of reads
Consensus quality: 20528 bases at least 040
Consensus quality: 205540 bases at least 030
Consensus quality: 205560 bases at least 020
Insert size: 205691; sum-of-contigs
Insert size: 188405; 91% error; agarose-fp
Quality coverage: 11.31x in 020 bases; sum-of-contigs Quality;
coverage: 12.57x in 020 bases; agarose-fp
                                                      NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALS83836.11 GI:14455940
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                   actgacettactggactactatettetetactgacattettggaaacatttcagggggtgg
                                                                                                                                                                                                                                                                                             88241 88340: gap of 100 bp
88341 205791: contig of 117451 bp in length
Location/Qualifiers
                                                                                                                                                                                                                                                                           697 ccatatettteattat-gagtetggttgttageteatgtgaagegggg 743
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------ Project Information
Center project name: bA466J14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: SC
Web site: http://www.sanger.ac.uk
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 10 clone
PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 205791)
Mashreghi-Mohammadi,M.
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AL583836/c
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Rabbit cytochrome P45011C4 (CYP2C4) gene, exons 2 and 3.
M74201
                                                                                                                                                                   12;
                                                                                                                                            Length 205791;
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                                                                                                                                                                   Indels
                                                                                                        100
                                                                                                                                                                    0; Mismatches 180;
/clone="RPI1-466J14"
/clone_lib="RPCI-11.2"
...88240
fragment_chain:1"
fragment_chain:1"
88341..205791
/note="assembly_fragment:01703
fragment_chain:1
clone_end:17
                                                                                                                                              Score 326; DB 2;
Pred. No. 5.5e-81;
                                                                                            vector_side:right"
38262 c 40890 g 69845 t
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Best Local Similarity
Matches 516; Conserva
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                         misc_feature
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RABP450112
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Human

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Submitted (24-MAR-1999) Laboratory of Pharmacology and Chemistry, National Institute of Envrionmental Health Sciences, 111 Alexander Drive PO Box 12233, Research Triangle Park, NC 27709, USA Location/Qualifiers
                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)
Klose, T.S., Blaisdell, J.A. and Goldstein, J.A.
Gene Structure of CYP2C8 and Extrahepatic Distribution of the Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cccadtgt--cagcttcctcttcttgcctgggatctcctcctagtttcgtttctcttc 457
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                                                                   12-APR-2000
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GAGGCCCGCTGCCTGGTGGAGGAGCTGAGAAAAACCAATGGTGG 531
                                                                                                                                                                                                                                                                J. Biochem. Mol. Toxicol. 13, 1-7 (1999)
2 (bases 1 to 463)
Close, T.S., Blaisdell, J.A. and Goldstein, J.A.
Direct Submission
                                                                     PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 264.6; DB 9;
Pred. No. 1.1e-63;
0; Mismatches 94;
                                                          HSBCYP2C04 463 bp DNA
Homo sapiens CYP2C gene, exons 2 and 3.
AF136833
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/db_xref="taxon:9606"
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/number=3
a 99 c 1
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                                                                                                            AF136833.1 GI:6707882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.69
Best Local Similarity 78.49
Matches 355; Conservative
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                                          RESULT 11
HSBCYP2C04
LOCUS
DEFINITION
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                  membrane protein;
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 71)

2 hao, J.; Chan, G.; Govind, S., Bell, P. and Remper, B.W.

Structure of 5' regions and expression of phenobarbital-inducible rabbit cytochrome P450IIC genes

DNA Cell Biol. 9, 37-48 (1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Gaps
                                                       Oryctolagus cuniculus (strain New Zealand White) adult liver Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 711;
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Pred. No. 4.8e-68;
0; Mismatches 110; Indels
 M74201.1 GI:165583
cytochrome P450 IIC4; drug metabolism; microsomal
monooxygenase.
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                                                                                                                                                                                           Location/Qualifiers
1. 711
/organism="Oryctolagus cuniculus"
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/cell_type="hepatocyte"
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/germline
                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
378. .527
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145 c 206 g
                                                                                                                                                                                                                                                                                                                                           /gene="CYP2C4"
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/number=3
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77.38;
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Muzny, D. M., Adans, C., Adio-Oduola, B., Ali-Osman, F. B., Allen, C., Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Banks, T., Barbaria, J., Bonnion, D., Bouce, J., Benneon, J., Binage, K., Blankehburg, K., Bonnio, D., Bouce, J., Burket, C., Burrell, K. L., Bonnio, D., Bouce, J., Burket, C., Burrell, K. L., Baryd, N. D., Carron, T. F., Cartor, M., Cavacos, S. R., Chacke, J., Chavez, D., Chavez, D., Chan, G., Carron, T. C., Cartor, D., Datonner, S. R., David, R., David, M., David, M., David, M., David, M., David, M., David, C., Ding, Y., Dinh, H. H., David, M., David, M., David, C., Ding, Y., Dinh, H. Douthwaite, R. J., Draper, H., Ford, J., Porger, P., Earlan, C., Edgar, D., Edgar, D., Edareris, C., Elhaj, C., Escotto, M., Falls, T., Earnhart, C., Edgar, D., Edareris, G., Dunn, A.L., Ding, Y., Dinh, H. H., Douthwaite, R. J., Draper, H., Ford, J., Forger, P., Gabisi, A., Gao, J., Garcia, A., Garrer, T., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garrer, M., Garrer, J., Foster, P., Frantz, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Huber, J., Hulyk, S., Hume, J., Jackson, E., Landry, N., Holloway, C., Harrins, M., Mapua, P., Martin, R., Martindel, A., Martinez, E., Mascey, E., Martiner, E., Maccho, R., Martinez, E., Mascey, E., Martiner, R., Martiner, E., Mascey, E., Martiner, E., Peter, A., Taber, A., Taber, M., Tanesy, J., Taylor, T., Telfford, B., Thomas, S., Usmani, K., Ward, Moure, C., Taylor, T., Telfford, B., Tong, S., Martiner, S., Wartiner, S., Wartiner, S., Wartiner,
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                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                             AC083888 147838 bp DNA HTG 01-APR-2001
Rattus norvegicus clone RP32-307N15, WORKING DRAFT SECUENCE, 21
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Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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Rattus norvegicus
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COMMENT

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NOIE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doss/Genbank_draft_data.html).

NOIE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                            sequencing vector: M13: L08821
Chemistry: Dye-primer Bodipy: 11% of reads
Chemistry: Dye-primer Bodipy: 11% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 133494 bases at least Q40
Consensus quality: 147276 bases at least Q30
Consensus quality: 147441 bases at least Q20
Estimated insert size: 136695; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: A.7x in Q20 bases; sum-of-contigs estimation
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            Sequencing vector: Plasmid; M77789
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         Annealing:
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PCR Cycles:
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                                                                                                               gaggatggaaaacagagacttacagagctcctcgggcagagcttggcccatccacatggc 397
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                                     Gaps
          Length 147838;
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Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                     Indels
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             DB 2;
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            Score 238.6; DB 2
Pred, No. 2.4e-56;
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STS sequence; primer;
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             32.1%;
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Unpublished (1995)
                         Best Local Similarity 69.9
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PCR profile:
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SOURCE
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Eucheria: Mortagoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae: Mus. Mus. I bases 1 to 168457)

Han JJ. Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R.

Gordon, M., Goltz, J.S. and Kucherlapati, R.

High Throughput Mouse Sequencing
Unpublished

C (bases 1 to 168457)
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Location/Qualifiers
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  degrees C for 15 seconds
degrees C for 23 seconds
degrees C for 30 seconds
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94 degrees C for 15
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Perkin Elmer 9600
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19 clone RP23-345G6
47 unordered pieces.
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5:

TITLE JOURNAL

COMMENT

AUTHORS

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29.9%; Score 221.8; DB 2; Length 168457;
65.2%; Pred. No. 1.3e-51;
ive 0; Mismatches 197; Indels 13; Gaps
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contig of 1951 bp in length
gap of unknown length
contig of 1501 bp in length
gap of unknown length
contig of 1239 bp in length
contig of 1139 bp in length
contig of 1105 bp in length
gap of unknown length
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of 3269 bp in length
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of 2746 bp in length
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of 2444 bp in length
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="19"
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Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Goltz, J.S. and Rucherlapati, R. Direct Submission
Submitted (11-NUG-2000) Department of Molecular Genetics, Albert Binstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
On Dec 28, 2000 this sequence version replaced gi:1199063).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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------Summary Statistics
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                                                                                                                                                                                                                                                                                                                      -----Genome Center
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                                                          Gene structure of cytochrome P-450(M-1) specifically expressed male rat liver
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                  atgacaaaatagtaac-ttcgtttgctgttatctctgtctactttcct----agctc
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lambda-[1,3,18,22,23,29].
Rattus norvegicus
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Sciurognathi: Muridae;
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Morishima,N., Yoshioka,H., Higashi,Y., Sogawa,K. and
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/note="P450 intron A"
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                                                                                               DB 10; Length 513;
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Pred. No. 2.4e-50;
0; Mismatches 123;
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ne: 7828 sec
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April 19, 2002, 08:08:00 ; Search time 232.27 Seconds (without alignments) 885.492 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pending_Patents_NA_New:*

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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ø			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	139.6	8.0	526	9	US-10-106-698-2440	Sequence 2440. Ap
7	137.2	7.9	591	9	-10-106-698	
E	59	3.4	465	9	-10-103-313	Sequence 627, App
4		3.0	1186	9	-313	
0	51.8	3.0	1186	9	US-10-105-299-7204	
9 0			1464	'n	US-09-559-013D-11	Sequence 11, Appl
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8 0	49	2.8	2026	ø	US-10-106-698-368	Sequence 358, App
6 0	49	2.8	13327	9	US-10-105-299-7201	Sequence 7201, Ap
10	45.8	5.6	1530	-	PCT-US02-06912-12	Sequence 12, Appl
11	45.8	2.6	1693	-	691	Sequence 8, Appli
12	44.6	2.6	254	'n	254	Sequence 18019, A
13	43.6	2.5	832	9	J-103-313-6	Sequence 625, App
14	43.6	2.5	1001	9	US-10-103-313-625	
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16	41.4	2.4	1182		US-10-103-313-522	622,
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-	41	2.3	583	9	US-10-102-806-124	124
c 19	41	2.3			3-313-6	96,
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21	40.8	2.3			US-09-975-254-11513	115
22	40.8	2.3			-2	Sequence 21714. A
23	40	2.3			-975-254-23	
24	39.4	. 2.3	237		9-975-254-14	Sequence 14003. A
25	6	2.3	2356		-103-313-10	103,
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LOCATION: (375)..(375)
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LOCATION: (387)..(387)
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2.2 1756 6 US-10-104-706-1 Sequence 2.2 253 5 US-09-975-254-13380 Sequence 2.1 261 5 US-09-975-254-19229 Sequence 2.1 265 5 US-09-975-254-23331 Sequence 2.1 267 5 US-09-975-254-19290 Sequence 2.1 745 6 US-10-103-313-102 Sequence 2.0 191 5 US-09-975-254-25520 Sequence 2.0 191 5 US-09-975-254-25520 Sequence	6 US-10-026-666-1 1 PCT-US02-06992-16 1 US-09-975-254-12971 1 PCT-US02-06912-4 6 US-10-103-313-100 5 US-09-575-254-24906 6 US-10-103-313-202 5 US-09-630-25 6 US-10-105-299-9415 6 US-10-106-698-3502 6 US-10-106-698-1347	SULI 1 10-105-698-2440 Sequence 2440, Application US/10106698 Sequence 2440, Application US/10106698 GENERAL INFORMATION: APPLICANT: Ruben et al. TITLE OF INVENTION Colon and Colon Cancer Associated Polynucleotides and Polyregrittle Reference: PA005P1 CURRENT APPLICATION NUMBER: US/10/106,698 CUBRENT FILING DATE: 2002-03-27 PRIOR FILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: PCT/VUS00/26524 PRIOR APPLICATION NUMBER: US 60/157,137	PRIOR PALICATION NUMBER: US 60/163,280 PRIOR PALICATION NUMBER: US 60/163,280 NUMBER OF SEQ 1D NOS: 8564 SOFTWARE: Petentin Ver. 3.0 SEQ 1D NO 2440 LENGTH: 526 TYPE: DNA ORGANISM: HOMO sapiens
	00 00 0 0 WW W W W A A A A A 1 W W C W W Q O — 1 S W A T U	RESULI 1 US-10-106-698-2440 Sequence 2440, A SEQUENCE 3440, A SEQUENCE 344	PRIOR APPL PRIOR FILI NUMBER OF SOFTWARE: SEO ID NO 2. LENGHH: 5 TYPE: DNA

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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUS/OYCI
CURRENT APPLICATION NUMBER: US/10/103.313
CURRENT FILING DAIE: 2002-03-12
NUMBER OF SEQ 1D NOS: 653
Prior Application removed - See File Wrapper or Palm; SOFIWARE: Fatentin Ver. 2.0
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Pred. No. 2.6e-26;
0; Mismatches 169; Indels
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LOCATION: (550)..(550)
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Best Local Similarity 58.59
Matches 238; Conservative
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 858
LENGTH: 591
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ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR PELING DATE: 1999-09-29
PRIOR PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8554
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57.5%; Pred. No. 5.9e-27;
live 0; Mismatches 176;
                  COCATION: (401)...(401)

OTHER INFORMATION: n equals a,t,g, or c, n MARE/RET: misc_feature
LOCATION: (414)

OTHER INFORMATION: n equals a,t,g, or c, n make/RET: misc_feature
LOCATION: (419)

OTHER INFORMATION: n equals a,t,g, or c, n make/RET: misc_feature
LOCATION: (419)

OTHER INFORMATION: n equals a,t,g, or c, n make/RET: misc_feature
LOCATION: (461)...(452)

OTHER INFORMATION: n equals a,t,g, or c, n make/RET: misc_feature
LOCATION: (468)...(488)

OTHER INFORMATION: n equals a,t,g, or c, n make/RET: misc_feature
LOCATION: (518)

OTHER INFORMATION: n equals a,t,g, or c, n make/RET: misc_feature
LOCATION: (518)

OTHER INFORMATION: n equals a,t,g, or c make/RET: misc_feature
LOCATION: (518)

OTHER INFORMATION: n equals a,t,g, or c make/RET: misc_feature
LOCATION: (523)

COTHER INFORMATION: n equals a,t,g, or c make/RET: misc_feature
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Best Local Similarity 57.5
Matches 238; Conservative
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US-10-103-313-627

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: TYPE: DNA
: ORGANISM: Mus musculus
US-09-559-013D-11
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; ORGANISM: Homo sapiens
US-10-105-299-7204
                      US-10-105-299-7204/c
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  Length 465;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ20721
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
FILOR APPLICATION removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
                                           0; Mismatches 193; Indels
Score 59.2; DB 6;
Pred. No. 2.5e-05;
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  Query Match 3.4%;
Best Local Similarity 47.6%;
Matches 175; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 1186
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GENERAL INFORMATION:
APPLICANT: Ono. TOSINIO:
1ILE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES
1ILLE OF INVENTION: THEREFOR
1ILLE OF INVENTION: THEREFOR
1ILLE OF INVENTION: UNMBER: US/09/559,013D
1CURRENT FILLE OF DATE: 1999-12-01
1CURRENT FILLNG DATE: 1999-12-01
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSen, et. al
ITILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/105,299;
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm: SOTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7204
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3.0%; Score 51.6; DB 5;
Best Local Similarity 44.0%; Pred. No. 0.00037;
Matches 329; Conservative 0; Mismatches 404;
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Best Local Similarity 55.2%
Matches 101; Conservative
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ttacttaaaaaaccttgcttttatggaaagtgatattttggagaaagtaaaagaacaccaa 751
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APPLICANT: Nakayama, Elichi
TITLE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: LO461/7086
CURRENT APPLICATION NUMBER: US/09/559,013
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 60/168,353
PRIOR FILING DATE: 1999-12-01
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SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 11, Application US/09559013
GENERAL INFORMATION
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; ORGANISM: Mus musculus
US-09-559-013-11
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Length 1464;

Score 51.6; DB 5; Pred. No. 0.00037;

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Ouery Match Best Local Similarity

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypep:
FILE REFERENCE: PA005p1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
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Mismatches 404; Indels
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SEQ ID NO 368
  Conservative
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US-10-106-698-368/c
Matches 329;
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; Sequence 7201, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; WUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SED ID NO 7201
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                                         FEATURE:
NAME/REY: misc_feature
LOCATION: (1326)..(1326)
COTHER INFORMATION: n equals a,t,g, or
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; ORGANISM: Homo sapiens
US-10-105-299-7201
LENGTH: 2026
TYPE: DNA
ORGANISM: Homo sapiens
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Ouery Match 2.8%; Score 49; DB 6; Length 13327; Best Local Similarity 56.5%; Pred. No. 0.0043; Matches 91; Conservative 0; Mismatches 70; Indels
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GENERAL INFORMATION:
TILLE OF INVENTION: Cytochrome P450s and Uses Thereof
FILE REFERENCE: 07678/100W03
CURRENT APPLICATION NUMBER: PCT/US02/06912
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 60/274,241
PRIOR APPLICATION NUMBER: US 60/275,597
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-03
SOFTWARE: FastSED for Windows Version 4.0
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Pred. No. 0.012;
0; Mismatches 277;
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Best Local Similarity 44.6%;
Matches 225; Conservative
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PCT-US02-06912-12
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LENGIH: 832
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                   Query Match
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GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Herk, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE: OF INVENTION: Plants
FILE REFERENCE: 38-21(15309)8
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
SEQ ID NO: 31255
SEQ ID NO 18019
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87 aaacteetetggeeceateeteteesagtgattggaaatateetaeagatagatatt 145
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                                                                                                                                                                                                                   APPLICANT: University of Kentucky Research Foundation III.E OF INVENTION: Cytochrome P450s and Uses Thereof; File REFERENCE: OF678/100w03
CURRENT APPLICATION UNBER: DCT/USO2/06912
CURRENT FILING DATE: 2002-03-08
PRIOR PELLING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-03
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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CORGANISM: Glycine max
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: TYPEMAITON: Clone ID: 700955037H1
TYPE: 254-18019
                                                         1359 attttacagaactttaacctgaaat 1383
                                                                                          1381 cttatacatggatttaactggtcat 1405
                                                                                                                                                                  PCT-US02-06912-8; Sequence 8, Application PC/TUS0206912; GENERAL INFORMATION:
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Best Local Similarity 51.7%;
Matches 104; Conservative
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58.6%; Pred. No. 0.033;
tive 0; Mismatches 64; Indels
Length 254;
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Sequence 626, Application US/10103313
Sequence 626, Application US/10103313
GENERAL INFORMATION:
SEQUENCE 626, Application US/10103313
STILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJ20701
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ 1D NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFIWARE: PatentIn Ver. 2.0
                                                      Indels.
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodi
FILE REFERENCE: PJZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed · See File Wrapper or Palm
SOFIWARE: Patentin Ver. 2.0
SEQ 1D NO 525
LENGTH: 1001
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Score 44.6; DB 5;
Pred. No. 0.011;
0; Mismatches 109;
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; GENERAL INFORMATION:
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Best Local Similarity 58.6%
Matches 95; Conservative
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US-10-103-313-626
                           Best Local Similarity
Matches 110; Conserv
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RESULT 15
US-09-975-254-16494
; Sequence 16494, Application US/09975254
; Sequence 16494, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molec:les Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molec:les Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molec:les Associated With
; TITLE OF INVENTION: NUMBER: US/09/975,254
; CURRENT APPLICATION NUMBER: US/09/263,191
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; WUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 16494
; LENGTH: 272
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                                                             2.5%; Score 43.6; DB 6; Length :001: 58.6%; Pred. No. 0.036; Astive 0; Mismatches 64; Indels 3
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Best Local Similarity 51.7%; Pred. No. 0.075;
Matches 93; Conservative 0; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                TYPE: DNA
CRGANISM: Glycine max
CHER INFORMATION: Clone ID: 700953251H1
08-09-975-254-16494
                                                                   Query Match
Best Local Similarity 58.6%
Matches 95; Conservative
; ORGANISM: Homo sapiens US-10-103-313-625
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Search completed: April 19, 2002, 11:06:02 Job time: 10682 sec

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Human; gene structure; phenotypic expression; guanosine cofactor; germline variation analysis; exon-intron boundary; Tetrahymena rRNA; cytochrome P450 2C19; CYP450 2C19; ds.
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/note= "Translation start site"
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Hursh cytochrome P
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score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.
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               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                    930621 seqs, 428662619 residues
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Database

Result Š.

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The present invention relates to a method for determining gene structure when the genomic sequence is unknown. The method involves sequencing the gene across soon intron boundaries using evenly spaced primers or tiled primers. The tiled primers comprises nucleic acids that hybridise to the known cDNA sequence of the gene at about 100-300 base intervals and the gene comprises the template. Gene structure can be determined without the need to sequence the entire gene. The method provides information necessary to determine gene structure and phenotypic expression without the need to sequence entire chromosomal copy of the gene or fragment. The methods are useful in germline sequence variation analysis. The method is also useful for determining the boundaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining structure of genes whose sequence is not known from cDNA, by sequencing the gene or gene across exon-intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the cDNA of gene
/bound_moiety= "Primer"
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between regions of nucleic acids that were separated by intervening sequence, and also for determining boundaries present in genes containing group 1 type intruors such as Tetrahymena TRNA, where self-splicing occurs in the presence of guanosine cofactor. The present sequence is human cytochrome P450 (CYP450) 2C19 gene related to the invention.
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                                                                                                Length 8437;
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                                                                 Sequence 8437 BP; 2392 A; 1501 C; 1541 G; 2654 T; 349 other;
                                                                                                                      Indels
                                                                                                 Score 622.6; DB 22;
Pred. No. 1.3e-183;
                                                                                                                         45;
                                                                                                                      0; Mismatches
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93.3%;
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                                                                                                                      Matches 694; Conservative
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biallelic markers. The sequences are related to various human genes incrosomal glutathione S-transferase II (MGSZII), malate decarboxylase enzyme (DMEI/MEI), cytochrome P450, glutathione genes including microsomal glutathione S-transferase II (MGSZII), malate decarboxylase enzyme (DMEI/MEI), flavin-containing monoxygenases (FMO), gamma-glutamyltransferase S (GGTS), dipeptidase (DP), glucose G-phosphate dehydrogenase (GFDH), phosphogluconate dehydrogenase (FMO), gluconase (GFDH), phosphogluconate dehydrogenase (FMO), alphosphate glucoronosyl transferases (UGT2). Each of these sequences contains a biallelic marker/polymorphism, which is represented in the sequence as a degenerate/undefined base. The genes to which the biallelic marker containing sequences are related are involved in drug metabolism. Sequences AAAHS1594 - AAAHS1598 represent the genomic sequence. AAB62205-AAB6206 are MGSTII gene and four alternative MGSTII cDNA sequences. AAB62205-AAB6206 are MGSTII gene products. PCR primers AAHS1599 and AAAHS1600 are used in an example for the amplification of human genomic DNA fragments. The invention includes a method of genotyping comprising determining the invention of an allele of a DME- or MGSTII related biallelic marker in population of an allele of a DME- or MGSTII related biallelic marker and phenotype, and to detect association between hablotype and phenotype and phenotype and to detect association between allele.
                                                           Human; biallelic marker; single nucleotide polymorphism: SNP; MGSIII: marcosomal glutathione S-transferase II; malate decarboxylase enzyme: DMEI; WEI; cytochrome P450; glutathione reductase; GSHR: GSHS; GGIS; flavin-containing monooxygenase; FMO; gamma-glutamyltransferase 5: flavin-containing monooxygenase; FMO; gamma-glutamyltransferase 5: phosphagaluconate dehydrogenase; GSPDH: haplotype: phosphogluconate dehydrogenase; PGDH: drug metabolism: phenotype: uridine diphosphate glucoronosyl transferase; UGIZ; asthma; hepatoxicity;
                   Human CYP2C8 related DNA containing a biallelic polymorphism SEQ ID 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or allele specific amplification assays. The method can be used to determine whether an individual suffers or is at risk of developing asthma or is at risk of developing hepatoxicity on treatment with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping .
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Sequence 1001 BP; 265 A; 185 C; 245 G; 305 T; 1 other;

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                                Gaps
58.4%; Score 433.6; DB 21; Length 1001; 77.3%; Pred. No. 4.3e-125;
                                ς.
                              0; Mismatches 164; Indels
                              Matches 577: Conservative
                 Similarity
 Query Match
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1 tragaaatatttgaagrottgtgtgctga-ataaaagratacaaatacaatgaaaaatato 59

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Human: biallelic marker; single nucleotide polymorphism; SNP; MGSTII; microsomal glutathione Stransferase II; malate decarboxylase entzyme; DMEI; MEI; cytochrome P450; glutathione reductase; GSHR; GGT5; flavin-containing monooxygenase; FMO; gamma-glutamyltransferase 5; flavin-giptochase; DFP, glucose 6-phosphate dehydrogenase; GFPBH; haplotype; phosphogluconate dehydrogenase; PGPH; drug metabolism; phenotype; uridine diphosphate glucoronosyl transferase; UGT2; asthma; hepatoxicity; Human CYP2C8 related DNA containing a biallelic polymorphism SEQ ID 50. 340 agitticiggaagaggcaattccccaatatctcaaagaattactaaaggactiggtaggi 399 359 350 cagagetectegggeagagettggeceatecacatggetgeceagtgt--eagetteete 417 477 577 537 637 597 697 657 757 717 tetteactagtgacgteettggaaacattteaggggtggecaggtetteattgcgcatec 817 400 gcacatatttctgtgtcagctttggtaactgggggtgagggggggtggaaaacagagcccta 459 atgetaaateaggettageaaatggacaaatagtaaettegtttgetgttatetetgte 119 578 caatggaaagaaggaaggagatccggcgtttctccctcacaaccttgcggaattttgg gatggggaagaggagcattgaggaccotgttcaagaggaagcccgctgccttgtggagga gttgagaaaaaccaagggtggtgaccctactccatatcactgaccttactggactacta gttgagaaaaaccaagggtgggtgactctactctgcgtcattgaccttaacagttacctg tettetetactgacattettggaaacattteagggggggggecatatetteattatgagte 460 aaaaagettele-ageagagettageetatelgeatggetgeeragtgttgeageaettte caatggaaagaaatggaaggagatccggcgtttctccctcatgacgctgcggaattttgg gatggggaagaggagtattgaggaccgtgttcaagaggaagctcactgccttgtggagga tactttcctagctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaac 240 agittictggaagaggcattticccactggctgaaagaggtaacagaggatttggtaggt gigcaigiccigiticagcaictgictiggggaigggaggaiggaaaaacagagactta 718 tgattgttagctcatgtgaagcaggg 743 818 tgattatcagcctcaggtggtggag AAH51159 standard; DNA; 1001 BP (first entry) W0200058508-A2 Homo sapiens. zileuton; ds 29-AUG-2001 05-0CT-2000 AAH51159; m 220 758 478 538 638 598 869 120 300 658 AAH51159 QQ qq a qq Ωp ò. QQ Ω 3 qq õ qq ò qq ò ò Ω ò Op ò ò ò 6

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                                                                                                                                                                                                                enzyme-related biallelic markers used for genotyping
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                                                                                                                                                                                                comprising sequences from
                                                                                                                                                                                                                                                Claim 13; Page 280; 673pp; English.
                                                                                                                                Bougueleret L,
              24-MAR-2000; 2000WO-IB00403.
                                              99US-0125259.
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                                              25-MAR-1999;
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flavin-containing monooxygenäse; FMO; gamma-glutamyltransferase 5; dipeptidase; DF; glucose 6-phosphate dehydrogenase; 66pDH; haplotype; phosphogluconate dehydrogenase; PGDH; drug metabolism; phenotype; uridine diphosphate glucoronosyl transferase; UGT2; asthma; hepatoxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAH51110-AAH51593 represent human DNA fragments which contain biallelic markers. The sequences are related to various human genes including microsomal glutathione S-transferase II (MGSTII), malate decarboxylase enzyme (DMEI/MEI), cytochrome P450, glutathione
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CYP2C9 related DNA containing a biallelic polymorphism SEQ ID 55
                                                                                                                                                                                                                                                                                                                                          Human; biallelic marker; single nucleotide polymorphism; SNP; MGSTII; microsomal glutathione S-transferase II; malate decarboxylase enzyme; DMEI; MEI; cytochrome P450; glutathione reductase; GSHR; GSHS; GGT5;
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301 acagagecetaaaaaagettete-ageagagettageetatetgeatgeetgecaagtgtt 359
                                                                                                                                                                          cggaattttgggatggggaagaggagcattgaggaccgtgttcaagaggaccgctgc
                                                                                                                                                                                                         479 cggaattttgggatggggaagargagcattgaggaccgtgttcaagaggaagctcactgc
                                                     cttgtggaggaggattgagaaaaaccaagggtgggtgaccctactccatatcactgacctta
                                    attottttcagcaatggaaagaaatggaaggagatccggcgtttctccctcatgacgctg
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cc reductase/synthase (GSHR/GSHS), flavin-containing monooxyge:ases (FWO), gamma-glutamyltransferase 5 (GGT5), dipeptidase (DP), glucose 6-phosphate dehydrogenase (GGPDH), phosphate dehydrogenase (FOBH), and uridine diphosphate glucoronosyl transferases (UGT2). Each of these sequences contains a biallelic marker/polymorphism, which is represented in the sequences as degenerate/undefined base. The genes to which the biallelic marker containing sequences are related are involved in drug metabolism. Sequences AAHSIS94 - AAHSIS98 represent the genomic sequence of the marker containing sequences are related are involved in drug metabolism. Sequences AAHSIS94 - AAHSIS98 represent the genomic sequence of the marker containing sequences. PCR primers AAHSIS99 and AAHSIS00-SAABSS906 are WGSTII gene and four alternative MGSTII cDNA sequences. AABSS906 are was method of genotyping comprising determining the invention includes a method of genotyping comprising determining the invention includes a method of genotyping comprising determining the constitution of an allele of a DME- or MGSTII related biallelic marker and population of an allele of a DME- or MGSTII related biallelic marker and considered and phenotype, and to detect association between haplotype and phenotype. The method is also used to detect association between haplotype and phenotype. The polyunclectides are used, in hybridization assays, sequencing assays or allele specific amplification assays. The method can be sed to asthma or is at risk of developing hepatoxicity on treatment with
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Sequence 436 BP; 100 A; 94 C; 105 G; 124 T; 13 other;

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                                                                                                                                                                                                                                                                                                                                                                                  61 tggacaaaatagtaacttertttgetgttawetetrtetactiteetagetetesaargt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cccactggctgaaagagctaacagaggatttggtaggtgtgcatgtgcctgttt~agcat 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctgtcttggggatggggaggatggaaaacagagcttacagagctcctcgggca:agctt 381
                                                                                 Gaps
                                                                                                                                                                                                                               9
                                                                                                                                                      22 giggcigaataaaagcatacaaatacaatgaaaatatcatgctaaatcaggcttagcaaa 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgaaghrgtgaaggaagccctgattgatcttggaagagagttttctggaagaggca*ttt
                                                                             ä
55.9%; Score 415.4; DB 21; Length 4.6; 96.3%; Pred. No. 1.3e-119;
                                                                             Indels
                                                                             2;
                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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ID AAD12247 standard: DNA; 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agtttcgtttctcttcc 458
                                                                             Matches 421; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 agtttcgtttctcttcc
                                        Similarity
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    Ouery Match
                                            Local
                                                                                                                                                                                                                                                                                                             82
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Human cytochrome P450 (CYP450) 2C19 gene PCR product #3.

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The present invention relates to a method for determining gene structure when the genomic sequence is unknown. The method involves structure when the gene across exon-intron boundaries using evenly spaced primers or tiled primers. The tiled primers comprises nucleic acids that principle to the known CDNA sequence of the gene at about 100-300 base intervals and the gene comprises the template. Gene structure can be certained without the need to sequence the entire gene. The method provides information necessary to determine gene structure and phenotypic expression without the need to sequence entire chromosomal copy of the canalysis. The methods are useful in germline sequence variation between regions of nucleic acids that were separated by intervening capence, and also for determining boundaries present in genes containing croup 1 type introns such as Tetrahymena rRNA, where self-splicing occurs in the presence of guanosine cofactor. The present sequence is a PCR product obtained from human cytochrome P450 (CYP450) 2C19 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining structure of genes whose sequence is not known from cDNA. by sequencing the gene or gene across exon-intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
          Human; gene structure; phenotypic expression; guanosine cofactor;
germline variation analysis; exon-intron boundary; Tetrahymena rRNA;
cytochrome P450 2C19; CYP450 2C19; ds.

    tcagaaatatttgaagcctgtgtggctgaataaaagcatacaaatacaatgaaaatatca

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 734 BP; 236 A; 170 C; 126 G; 199 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 369; DB 22;
Pred. No. 5.3e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 4; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.78;
                                                                                                                                                                             17-JAN-2001; 2001WO-US01461.
                                                                                                                                                                                                           2000US-0488127
                                                                                                                                                                                                                                                                             Fitzgerald MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 427; Conservative
                                                                                                                                                                                                                                                                                                           WPI; 2001-465380/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                           W0200153529-A2
                                                                                Homo sapiens.
                                                                                                                                                                                                           20-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                             of gene
                                                                                                                                                                                                                                                                             Thomann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408
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The present invention relates to a method for determining gene structure when the genomic sequence is unknown. The method involves sequencing the gene across exon-intron boundaries using everly spaced primers or tiled primers. The tiled primers comprises nucleic acids that hybridise to the known cDNA sequence of the gene at about 10.300 base intervals and the gene comprises the template. Gene structure can be determined without the need to sequence the entire gene. The method provides information necessary to determine gene structure and phenotypic expression without the need to sequence entire chromosomal copy of the gene or fragment. The methods are useful in germline sequence avaiation analysis. The method is also useful for determining the boundaries between regions of nucleic acids that were separated by intervening sequence, and also for determining boundaries present in genes containing group 1 type introns such as Tetrahymena rRNA, where self-splicing occurs in the presence of gunnosine ocfactor. The present sequence is a PCR product obtained from human cyclochrome P450 (CYP450) 2019 gene
                  tgcatgtgcctgtttcagcatctgtcttggggatggggaggatggaaaacagagggcttac 360
                                                                          420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining structure of genes whose sequence is not known from cDNA, by sequencing the gene or gene across exon-intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the
                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene structure; phenotypic expression; quanosine coiactor; germline variation analysis; exon-intron boundary; Tetrahymena rRNA; cytochrome P450 2C19; CYP450 2C19; ds.
                                                                                       111 AGAGCTTCTCGGCCAGAGCTTGCCCATCCACATGGCTGCCCAGTGTCAGCTTCTTTT
                                                                       agagetectegggeagagettggeecatecacatggetgeecagtgteagettertet
                                                                                                                                        Human cytochrome P450 (CYP450) 2C19 gene PCR product #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 557 BP; 119 A; 107 C; 137 G; 167 T; 27 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 4; 81pp; English.
                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                   557
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                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                AAD12245 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomann H, Fitzgerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-465380/50.
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301
                                                                     361
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Score 366.2; DB 22; Length 5^r Pred. No. 3.4e-104;

49.88;

Query Match Best Local Similarity

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518
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                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by sequencing the gene of genes whose sequence is not known from cDNA, by sequencing the gene or gene across exon-intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the CDNA of gene
                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human: gene structure; phenotypic expression; guanosine cofactor; germline variation analysis; exon-intron boundary; Tetrahymena rRNA; cytochrome P450 2C19; CYP450 2C19; ds.
                                                                                                                                                                                                                                                                                     579 cccgctgccttgtggaggagttgagaaaa--ccaagggtgggtgaccctactccatatc
                                                                                                                                                                                                                                                                                                                                 219 ccctgattgatcttggaggagagttttctggaagaggcattttcccactggctgaaagag
                               ctaacagaagatttggtaggtgtgcatgtgcctgtttcagcatctgtcttggggatgggg
                                                                                                                                                                                                tgttaggaattgttttcagcaatggaaagaaatggaaggagatccggcgtttctccctca
                                                                                                                                                                                                                     240 tqttaggaatcgttttcagcaatggaaagagatggaaggaggatccggcgtttctccctca
                                                                                                                                                                                                                                          519 tgacgctgcggaattttgggatggggaagaggagcattgaggaccgtgttcaagaggaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for determining gene
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytochrome P450 (CYP450) 2C19 gene PCR product #4.
  45;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 4: 81pp; English
0;
                                                                                                                                                                                                                                                                                                                                                                                                               BP,
                                                                                                                                                                                                                                                                                                                                                                                                             AAD12249 standard; DNA; 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-2000; 2000US-0488127
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thomann H, Fitzgerald MS;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-465380/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-2001
Matches 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD12249;
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                                                                279
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Disclosure: Column 55-56; 91pp; English.

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sequencing the genomic sequence is unknown. The method involves sequencing the gene across exon-intron boundaries using evenly spaced primers or tiled primers. The tiled primers comprises nucleic acids that hybridise to the known cDNA sequence of the gene at about 100-300 base intervals and the gene comprises the template. Gene structure can be intervals and the gene comprises the template. Gene structure can be provides information necessary to determine gene structure and phenotypic expression without the need to sequence entire chromosomal copy of the gene or fragment. The methods are useful in germline sequence variation analysis. The method is also useful for determining the boundaries between regions of nucleic acids that were separated by intervening sequence, and also for determining boundaries present in genes containing in the presence of guanosine cofactor. The present sequence is a PCR product obtained from human cytochrome P450 (CYP450) 2019 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and 367U primer related to the invention.
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Sequence 570 BP; 146 A; 101 C; 142 G; 178 T; 3 other;

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Gaps
            ij
26.0%; Score 193.2; DB 22; Length 570; 93.8%; Pred. No. 3.4e-50;
            Indels
                                                                                               Pred. No. 3.4e
0; Mismatches
            Conservative
     Local Similarity es 212; Conserv
Query Match
      Best Loca
Matches
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Cytochrome P450; detergent; enzyme inhibitor; non-ionic; ionic; purification; drug oxidation; steroid; carcinogen; pesticide: human;
                                                  Human cytochrome P450 2C10 variant DNA.
      AAX22716 standard; DNA; 1419
                                                                                                                                    94US-0194981
                                   (first entry)
                                   27-MAY-1999
                                                                                       Homo sapiens
                                                                                                                                   10-FEB-1994;
                                                                                                      US5886157-A
                                                                                                                    23-MAR-1999
                     AAX22716;
AAX227
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Purifying recombinant cytochrome P450 - by utilising momentoons of detergents and enzyme inhibitors Sandhu P; 7, Gno Gillam EMJ, Guengerich FP, WPI; 1999-228609/19.

94US-0194981

LO-FEB-1994;

(UYVA-) UNIV VANDERBILT.

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This invention describes a recombinant cytochrome P450 protein which is purified from a host cell culture using a combination of detergents and enzyme inhibitors. The method comprises (a) fractionating the host cells to prepare their membranes, (b) adding a non-ionic detergent to the membranes in a concentration of 0.8% to 2% (w/v) in a detergent:protein ratio of between 4:1 to 10:1, (c) adding an ionic detergent:protein ratio of between 4:1 to 10:1, (c) adding an ionic detergent:protein ratio of between 2:1 to 4:1 (d) centrifuging the membrane-detergent ratio of between 2:1 to 4:1 (d) centrifuging the membrane-detergent ratio of between 2:1 to 4:1 (d) centrifuging the membrane-detergent ratio of between 2:1 to 4:1 (d) centrifuging the protein ratio of between 2:1 to 4:1 (d) centrifuging the contribution of the protein through a diethylaminocathyl-beaded column, then through a carboxymethyl-beaded column, and finally through a hydroxylapatite column. The method is used to purify cytochrome P450 proteins which are responsible for catalysing the oxidation of drugs, steroids, carcinogens and pesticides. The method simplifies the purification of P450 proteins, by the use of improved expression vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1419 BP; 409 A; 332 C; 307 G; 371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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Pred. No. 1.5e-40;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and novel detergent combinations.
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97.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 97.17
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186
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primer; expression vector; protein; metabolite; Human cytochrome P450 molecular species 2C9 cDNA. Human cytochrome P450; amplification; PCR; yeast NADPH-P450 reductase; safety; fusion carcinogen; mutagen; liver metabolism; ds. (HAYA/) HAYASHI K. (SUMO) SUMITOMO CHEM CO LID. 93JP-0180246. 93JP-0201120. 93JP-0208279. 94EP-0111298 Homo sapiens. 20-JUL-1994; 21-JUL-1993; 20-JUL-1993; 30-JUL-1993; 22-MAR-1995. EP644257-A.

AA087715 standard; cDNA; 1473 BP.

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AA087715

(first entry)

10-NOV-1995

AAQ87715:

Sakaki T;

Nakatsuka I,

Komai K,

Kaneko H,

Hayashi K, Yabusaki Y;

WPI; 1995-116991/16. P-PSDB; AAR72361.

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(SUMO ) SUMITOMO CHEM CO LID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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                                                                  The nucleotide sequence of the cDNA encoding the human cytochrome F450 was amplified by PCR using the prient of 491 amino acids. The CDNA was amplified by PCR using the prients AA087735. The product was cloned into the yeast expression vectors pAAHSN or pAHRR to produce the vectors p2C9 for the expression of the cytochrome P450 alone or p2C9R for co-expression with the yeast NADPH*P450 reductase.

The vectors are used in a method for evaluating the safety of a chemical roompound by reacting the chemical compound with recombinantly produced human cytochrome P450 molecular species 1A2 (AA087714), 2C9, 2E1 (AA087716) or 3A4 (AA087710), or their auxillary species and variants (AA087716) or 3A4 (AA087717), or their auxillary species and variants or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound, or its metabolite, will be converted into metabolite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;
evaluation; safety; fusion protein; metabolite; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                            126 cctagctctcaaaggtctatggcctgtgttcactctgtattttggcctgaaacccatag 185
                                                                                                                                                                                                                                                                                                                                                                                      164 ccaatctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 223
                                                                                                                                                                                                                                                                                                                                         Gars
              Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
                                                                                                                                                                                                                                                 a carcinogenic or mutagenic form through metabolism in the liver
                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                             Score 163; DB 16; Length 1473;
Pred. No. 1.5e-40;
0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1473 BP; 413 A; 345 C; 319 G; 395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cytochrome P450 molecular species 209 gene.
             Evaluation of safety of a chemical cpd. - using
                                                Examples; Page 23-25; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT28381 standard; DNA; 1473 BP
                                                                                                                                                                                                                                                                                                             Ouery Match 21.9%;
Best Local Similarity 97.1%;
Matches 166; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMO ) SUMIIONO CHEM CO LID.
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93JP-0208279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-182311/19.
P-PSDB; AAR93168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carcinogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1994;
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This is the nucleotide sequence of the human cytochrome P450 molecular species 2C9 gene which encodes a protein of 490 amino acids. The gene was amplified from a human liver derived cDNA library as 2 fragments of 0.9 and 0.6 kb using primers AA128915-8. The prod. was cloned into the yeast expression vector pAA45N to generate plasmid p2C9 for prodn. of the cytochrome only or into the vector pAA45N to generate plasmid p2C9 for prodn. of the cytochrome only or into the vector pAA45N to generate the plasmid p2C9 for co-prodn. with the yeast NAD9H-P450 reductase. The sequence is placed under control of the yeast ADH gene promoter and terminator. The vectors are used in a method for evaluating the safety of a cpd. by reacting the test cpd. with recombinantly produced human cytochrome P450 mol. species 1A2 (AA128880), 2C9, 2E1 (AA128832), 3A4 (AA128833) or their variants (AA128880), 2C9, 2E1 (AA128382), 3A4 (AA128383) or eductase (either as a fused protein or as a cell extract) and analysing the resultant metabolite. The cpd. is considered "safe" if it is not detoxified or is metabolised to a carcinogenic or "unsafe" if it is not detoxified or is metabolised to a carcinogenic cor "unsafe" if it is not detoxified or is sequence 1473 BP; 413 A: 345 C: 319 G: 396 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NADPH reductase to determine whether the analyte cpd. is detoxified or metabolised to a carcinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human derived cytochrome; P4502C9; commercial cDNA library; yeast; transfection; recombinant production; expression vector; mammal; immunisation; sensitisation; antibody; determination; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.9%: Score 163; DB 17; Length 1473; 97.1%; Pred. No. 1.5e-40; i::e 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 20-22; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human derived cytochrome P4502C9 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 97.17
Matches 166; Conservatire
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP08027196-A.
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in purified from a host call culture using a combination of detergents and enzyme inhibitors. The method comprises (a) fractionating the host cells to prepare their membranes, (b) adding a non-ionic detergent to the membranes in a concentration of 0.8% (w/v) in a detergent: protein ratio of between 4:1 to 10:1, (c) adding an ionic detergent to the membranes in a concentration of 0.8% to 0.8% (w/v) in a detergent:protein ratio of between 7:1 to 4:1 (d) centrifying the membrane detergent mixture to remove insoluble materials and (e) membrane-detergent mixture to remove insoluble materials and (e) through a carboxymethyl-beaded column, then through a carboxymethyl-beaded column, and finally through a disthylaminoethyl-beaded column, then through a carboxymethyl-beaded column, and finally through a hydroxylapatite column. The method is used to purify cytochrome P450 proteins which are responsible for catalysing the oxidation of drugs, steroids, carcinogens and pesticides. The method simplifies the purification of P450 proteins, by the use of improved expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 cctagctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New P450 fusion proteins—comprising a portion of a bacterial sytochrome P450 protein and a portion of a mammalian sytochrome P450.
This invention describes a recombinant cytochrome P450 protein which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacterial; mammalian: cytochrome P450; chimeric; fusion protein; oxidise; hydrocarbon; carbon-hydrogen bond; hydroxylating; bioremediation; environmental pollutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                       21.9%; Score 163; DB 20; Length 1591; 97.1%; Pred. No. 1.6e-40; ive 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 ctggaagaggcattttcccactggctgaaagagctaacagaggatttggta 296
                                                                                                                                                                                                                                                                                                                                                          Sequence 1591 BP; 443 A; 372 C; 353 G; 423 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalian cytochrome P450 protein CYP2C9 encoding DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 165; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY04127.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytochrome P450; detergent; enzyme inhibitor; non-ionic; ionic; purification; drug oxidation; steroid; carcinogen; pesticide; human: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                             The present sequence encodes the human derived cytochrome (HDC) P45029, which was obtd. from a commercial cDNA library. Yeast were transfected with an expression vector contg. the HDC cDNA. Library toultured and then disrupted to give a microsomal fraction. The HDC was purified from the fraction, and used to immunise and sensitise a mammal. Blood was drawn from the mammal, and an anti-HDC antibody isolated. The antibody obtd. recognises HDC P4502C9, partic. at a serum dilution rate of 1:10000, and is substantially without cross reaction to other HDC P450 spp..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                            Antibody recognising human derived cytochrome P4502C9 - allows specific detection of cytochrome P450 species in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
21.9%; Score 163; DB 17; Length 1473;
Best Local Similarity 97.1%; Pred. No. 1.5e-40;
Matches 166; Conservative 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1473 BP; 413 A; 345 C; 319 G; 396 I; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purifying recombinant cytochrome P450 · by utilising combinations of detergents and enzyme inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sandhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 53-54, 91pp; English
                                                                                                                                           Example 1; Pages 11-13; 13pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytochrome P450 2C10 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX22715 standard; DNA; 1591
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               WPI; 1996-136337/14.
P-PSDB; AAR81465.
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AAX22715;

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The present invention describes a fusion proteins comprising a portion of a bacterial cytochrome P450 protein and also a portion of a mammalian cytochrome P450 protein. The fusion protein can oxidise hydrocarbons or any compound having a carbon-hydrogen bond. The fusion protein can be used for hydroxylating a compound to be oxidised. It can also be used in the bioremediation of an environmental pollutant. Since the fusion protein is soluble, it can be subject to structural elucidation by X-ray crystallography for designing functional proteins. It can be readily expressed in soil bacteria to facilitate bioremediation. The present sequence encodes mammalian cytochrome P450 protein CYP2C9 from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome P450 2C19; human; liver; PCR; primer: detection: CYP2C19; stereospecific S-mephenytoin 4'-hydroxylase activity; polymorphism; ss.
                                                                                                                                                                                                                                                             cctagctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 185
                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                         21.9%: Score 163; DB 20; Length 1845; 97.1%: Pred. No. 1.7e-40; ive 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                      246 ctggaagaggcattttcccactggctgaaagagctaacagaggatttggta 296
                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                    Sequence 1845 BP; 507 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= Cytochrome P450 C9 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytochrome P450 2C9 clone 65 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= b
/~note= "Variable position"
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"Variable position"
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11..1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT11381 standard; cDNA; 1852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , 95WO-US05744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0238821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-1996 (first entry)
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                                                                                                                                                                                                                                       Matches 166; Conservative
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P-PSDB; AAR89865.
                                                                                                                                                                                                                          Similarity
                                                                                                                                              present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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The sequences given in AATI1378-81 encode allelic variants of cytochrome 450 209. The majority of clones isolated from liver S33 coded for 209. Of the 50 clones encoding 209, only two allelic variants were found. 39 cof the 209 clones were identical with clone 65, and 11 were identical cartial states were found. 39 cof the 209 clones were identical with clone 65, and 11 were identical cartial states of the 209 clones but contained 2 single base changes at positions 30 clone 25. Clone 25 and 62 single base changes at positions 20 clones 29c and 60 differ by one nuclectide in the coding region. The clones 29c and 60 differ by one nuclectide in the coding region clones 29c and 60 differ by one nuclectide in the coding region. The cartial state is a single amino acid change. The to Met at position 385. Clone 29c has a very long, 198 bp, 5'-noncoding region and a polyadenylation signal 21 bases from the poly-A tail. Clone 6b chas an unusually long 3'-noncoding region containing three possible color signals with no poly-A tail. The differences in the 3' con-coding regions could represent alternate splicing, allelic variants of 2018 because they differ by only one base in the coding region. They are most similar to 209 (82% amino acid homology).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 cctagctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytochrome P450: drug screening; S-mephenytoin 4'-hydroxylase; identification; mutagenic; carcinogenic; cytotoxic; haemoprotein; xenobiotic; environmental pollutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 ccaatctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 163; DB 17; Length 1852; Pred. No. 1.7e-40;
         New isolated cytochrome P450 2C subfamily member - used for identifying drugs metabolised by S-mephenytoin 4'-hydroxylase activity and to develop other screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1852 BP; 514 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cytochrome P450 2C9 clone 65 cDNA.
                                                                                    Example 2: Page 104: 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР
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97.1%;
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92US-0864962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.9
Best Local Similarity 97.1
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1994;
09-APR-1992;
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                                                                                                                                                         This sequence encodes a human cytochrome P450 2C9 polypeptide isolated from clone 65. This polypeptide is used in a method to screen for a drug that is metabolised by a cytochrome P450 having S-mephenytoin 4'-hydroxylase activity. The protein can also be used to identify a mutagenic, carcinogenic or cytotoxic compound. Cytochrome P450 are a large family of hemoprotein enzymes capable of metabolising xenobiotics such as drugs carcinogens and environmental pollutants as well as endoblotics such as steroids, fatty acids and prostaglandins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                    Screening for drugs metabolised by cytochrome P450 - for identifying mutagenic, carcinogenic, or cytotoxic compounds
                                                                                                                                                                                                                                                                                                                                                                          ::
                                                                                                                                                                                                                                                                                                                                         Length 1852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 163; DB 19; Length 1.
Pred. No. 1.7e-40;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                Sequence 1852 BP; 514 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                Example 2; Column 53-56; 63pp; English.
                            Romkes-sparks M;
                                                                                                                                                                                                                                                                                                                                          21.98;
97.18;
                                                                                                                                                                                                                                                                                                                                         Query Match 21.95
Best Local Similarity 97.15
Matches 166; Conservative
(ROMK/) ROMKES-SPARKS M.
                                                      WPI; 1998-436528/37.
                            Goldstein JA,
                                                                                                                                                                                                                                                                                                                                                                                                      126
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BGG17892 602645541
AV660643
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BG563317 602582203
BG569317 60258622
T53976 yb85f11.s1
AV697373 AV697373
AV697578 AV697373
AV694577 AV694577
AV661103 AV656121
AV661103 AV656120
AV649200 AV649200
AV64920 AV649415
AV661158 AV661158
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AV687011 AV687011
AV655255 AV655255
AV650504 AV650504
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                                                                                                                                                                             AV691273 A
                                                                                                                                                                                           AV688076
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKCBJD11"
/clone_lib="GKC"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hanzq@chgc.sh.cn
This clone is available at CHGC in Shanghai
                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                         AV661559
AV661295
AV661281
                                                                                                                                                                              AV691273
AV691272
AV688076
AV690361
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AV655255
AV650504
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AV653206
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AV649200
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AV647944
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  human.
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257.4
253.2
249.8
245.6
225.8
225.8
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ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                              RESULT
AV683520
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  SOURCE
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                                            April 19, 2002, 08:07:44; Search time 2723.34 Seconds (without alignments) 2931.736 Million cell updates/sec
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AV693304 AV693304
AV697314 AV695314
AV697317 AV697749
AV697538 AV697837
AV696639 AV697639
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                       11351937 seqs, 5372889281 residues
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Listing first 45 summaries
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AV697749
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AV693304
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324.2 322.8 322.8 322.8 321.8 321.8 321.8 321.8

Score

Result Š.

AV688076

AV691273 AV691272

Minimum DB seq Maximum DB seq

Database

Perfect score:

Sequence:

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 628)

1 (bases I to 628)

2 Wu,T., Olan,B., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,S., Li,N., Peng,Y., Liu,F., Ou,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.

1 Homo sapiens CDNA GR- clones

1 Homo sapiens CDNA GR- clones

1 Homo sapiens CDNA GR- clones

2 Unpublished (2000)

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Fax: 86-21-50801922

Email: hanz@ehgc.sh.cn

This clone is available at CHGC in Shanghai.
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Site_2:
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mRNA sequent
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AV693304 GKC Homo sapiens cDNA clone GKCBIB04 5', a
AV693304
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/note="Vector: pBluescript sk(-);
                                                                                   0; Mismatches 113;
                                                              Score 324.2; DB Pred. No. 2e-78;
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                     165
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Best Local Similarity 78.2%;
Matches 415; Conservative 0
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Homo sapiens
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Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

Mu, T., Qian, B., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,

Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, I.,

Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang

Y., Gu, Y., Chen, Z. and Han, Z.

Hamo sapiens CDNA GK- clones
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AV655514 GKC Homo sapiens cDNA clone GKCBID04 5', mRNA sequence.
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                                                                             carcinoma'
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Pred. No. 4.7e-78;
); Mismatches 117;
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GRCBIB04"
/clone=Lib="GRC"
/tissue_Lype="hepatocellular ca/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-xhol"
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144 C
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  Homo sapiens
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              Contact: Zeguang Han
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Tel: 86-21-50801291
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/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_l:
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Pred. No. 4.7e-78;
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Matches 416; Conservative
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Enterporation Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Lot 692)

1 (bases 1 to 692)

1 (bases 1 to 692)

2 (v. 1. dian.B., Huang, O., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.

Homo sapiens cDNA GK- clones

Unpublished (2000)

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Tel: 86-21-50801929 (ex. 45)

Fax: 86-21-50801929 (ex. 45)
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                                                                                                                                                                                                                                                                                                                                                                                                               1 692
/ Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKCBIF10"
/clone_lib="GKC"
/tissue_type="hepatocellular ca/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                       Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butheria; Butheria; Primates; Catarrhin!; Hominidae: Homo.

(bases 1 to 651)

Wu,T., Olan, B., Homorg,O., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,M., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang, Y., Gu,Y., Chen,Z., and Han,Z.

Homo sapiens cDNA GK- clones

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript sk(-); Site_1: EcoR1: Site_2:
                                                                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
551 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudosy, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                         25-SEP-2000
mRNA sequence.
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               AV697837 GKC Homo sapiens cDNA clone GKCBFC05 5'. AV697837
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/dev_stage="Adult"
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Location/Qualifiers
1, .651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 321.8; DB 10;
Pred. No. 9e-78;
0; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185
                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 g
                                                                                                                                                                                                                                                                                                                                                                                                     /clone="GKCBFC05"
/clone_lib="GKC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="SOLR"
                                                               AV697837.1 GI:10299700
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                                                                                           human
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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RESULT
AV697837
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Homo sapiens
Eukaryota, Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi:
Eukaryota, Metazoa: Chordata: Catarrhini: Hominidae: Homo.

1 (bases 1 to 675)
Wu T. (Jian, B., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,
Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang
Y., Gu, Y., Chen, Z. and Han, Z.
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Eax: 86-21-508019122
Email: hanzg²chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                           AV696436 675 bp mRNA EST 25-SEP-2000
AV696436 GKC Homo sapiens cDNA clone GKCBJA05 5', mRNA sequence.
AV696436.1 GI:10298299
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                                 479
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gatccggcgtttctccctcatgacgctgcggaattttgggatggggaagaggagcattga
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                                                                   Length 675;
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/organism="Homo sapiens"
/db.ref="taxon:9606"
/clone="GKCBJA05"
/clone_lib="GKC"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
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9e-78;
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Pred. No. 9e-78;
0; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Matchass 43.3%;
Best Local Similarity 77.4%;
Matches 415; Conservative (
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AUTHORS
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Query Match
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AUTHORS
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi:

Hobses 1 to 67)

RS W.T., Olan.B., Huang,O., Huang,C., Kang,B., Gao.X., Xu,Z., Xiao.H.,

Xu,X., Li,N., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,H., Cheng,Z., Zeng,L.,

Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,

Y., Gu,Y., Chen,Z. and Han,Z.

Homo sapiens CubA GK- clones

(Npublished (2000)

Contact: Zeguang Han

Contact: Seguang Han

Contact: Seguang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV697538 677 bp mRNA EST 25-SEP-2000
AV697538 GKC Homo sapiens cDNA clone GKCBJB03 5', mRNA sequence.
AV697538
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                                                                                                                                241 TTGGTAACTGGGGTGAGGGGGATGGAAAACAGAGCCCTAAAAAGCTTCTC-AGCAGAGCT 299
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/dev_stage="Adult"
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Pred. No. 9e-78;
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/db_xref="taxon:9606"
/clone="GRCBJB03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV697538.1 GI:10299401
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ilarity 77.4%;
Conservative
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JOURNAL
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutearyota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 677)

S Wu,T., Ojan, B., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Cau, Y., Chen, Z. and Han, Z.

Homo sapiens cDNA GK- clones

Unpublished (2000)

Contact: Zequang Han Genome Center at Shanghai

Si Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Tel: 86-21-50801919(ex.45)
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5', mRNA sequence.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                         360
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                                                                                                                                                                                                                                                                                                                                                                                                 182 CCCCAATATCICAAAGAATTACTAAAGGACTIGGIAGGIGCACAIATTICIGIGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GRCBJC11"
/clone_lib="GRC"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV698646 677 bp mRNA EST
AV698646 GKC Homo sapiens cDNA clone GKCBJC11
AV698646 1 GI:10300617
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
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1 (bases 1 to 680)

2 Wu,T., Qian,B., Huang,O., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M. Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.

Homo sapiens cDNA GK- clones

Unpublished (2000)

Contact: Zequang Han

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201203, P. R. China

Tel: 86-21-50801929

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript sk(-); Site_1: Ecof1; Site_2:
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                                                                                                                     260
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                                                                                                                                                                                                                                            380
                                                                                                                                                                                                                                                         242 IIGGTAACIGGGGIGAGGGAAAACAGAGCCCIAAAAAGCIICI-AGAGAGCI 300
                                                                                                                                                                                                                                                                                                      381 tggcccatccacatggctgcccagtgt--cagcttcctctttcttgcctgggatctcct 438
                                                                                                                                                                                                                                                                                                                      atggacaaaatagtaacttcgtttgctgttatctctgtctactttcctagctctcaaagg 140
                                                                                        121
                           61
                                                                                                                cctagitticgitticiticitgitiaggaatigitticagcaatggaaagaaatggaaagga
                                                                        62 TCTATGGTCCTGTGTTCACCGTGTATTTTGCCATGATCCCATAGTGGTGTTTCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ACGAGCACCAATGTAAGTCTGCCTTATGTTCCTCCAGCCAATTGCAAAGGTTCTCAAAAG
                                                         141 tctatggccctgtgttcactctgtattttggcctgaaacccatagtggtqctqcatggat
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/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKCBIE09"
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JOURNAL
COMMENT
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AUTHORS
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AV696639
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Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Manmalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 622)

Wu,T., Olan,B., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,

Xu,X., Li,N., Peng,Y., Liu,F., Ou,J., Song,H., Cheng,Z., Zeng,L.,

Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang, Homo sapiens cDNA GK- clones

Unpublished (2000)
                                                                                                                5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV697579 6ZC bp mRNA EST 25-SEP-2000
AV697579 GKC Homo sapiens cDNA clone GKCBJB12 5', mRNA sequence.
AV697579.1 GI:10299442
                                                                                                                                                                                                                             261 teceactggetgaaagagetaacagaggatttggtaggtgtgeatgtgeetgttteagea 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309
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Location/Qualifiers
                                                                         Score 317; DB 10; I
Pred. No. 1.9e-76;
O; Mismatches 121;
  ų
  192
  6
167
                                                                         Query Match 42.7%;
Best Local Similarity 76.9%;
Matches 412; Conservative
141 c
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EWATYOLE: Buteleostomi:

EWATYOLE: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

EUKATYOLE: Metazoa: Chordata: Catarrhini: Hominidae: Homo.

I (Bases 1 to 646)

Wu,T., Olan, B., Huang, C., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,

Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,

Xu,X., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chong.Z. and Han,Z.

Y., Gu,Y., Chon,Z. and Han,Z.

Homo sapiens cDNA GR- clones

Ungublished (2000)

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801919(ex.45)

Email: hanzq@chgc.sh.cn
                                                                                                                              1. 747

// Organism="Homo sapiens"

/db_xref="taxnon:9606"

/clone="dlcATD11"

/clone="lb="dlc"

/tissue_type="Adult"

/dev_stage="Adult"

/lab_host="SoLR"

/note="Wector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 Contact: Zeguang Han
Contact: Zeguang Han
Contocs National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Eax: 86-21-50801922
Email: hansq4pqc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV696485 GKC Homo sapiens cDNA clone GKCBJA12 5', mRNA sequence.
AV696485. GI:10298348

    tcagaaatatttgaagcctgtgtgtggctgaataaaagcatacaaatacaatgaaaatatca

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0
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Pred. No. 6.5e-69;
); Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                2 others
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Bukaryota, Metazoa: Chordata; Craniata: Vertebrata; Buteleostomi;

Bukaryota, Metazoa: Chordata; Catarrhini: Hominidae; Homo.

1 (bases 1 to 747)

Qian, B., Wu, T., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Qu, J., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu Homo sapiens cDMA clone
Unpublished (2000)
1. .622
/drganism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKCBJB12"
/clone="GKCBJB12"
/tissue_itype="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoR1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV646984 747 bp mRNA ESI 07-SEP-2000 AV646984 GLC Homo sapiens cDNA clone GLCATD11 3', mRNA sequence. AV646984
                                                                                                                                                                                                                                                                                                                                                                                                                                       250
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                                                                                                                                                                                                        Length 622;
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Pred. No. 7.5e-76;
0; Mismatches 122; Indels
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Best Local Similarity 76.7%;
Matches 411; Conservative
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AUTHORS
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location/Qualifiers
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/clone= GRCBJA12*
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/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SQLM"
/lab_host="SQLM"
/note="Vector: pBluescript sk(-): Site_1: EccRI; Site_2:
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1 (bases 1 to 721)
NHI-MGC http://mgc.nci.nih.gov/.
NAtional Institutes of Health, Mammalian Gene Collectio:: (MGC)
Unpublished (1999)
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602645541F1 NIH_MGC_76 Homo sapiens CDNA clone IMAGE:4755890
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:476699"
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/clone="IMAGE:47699"
/clone="IMAGE:47699"
/clone="IMAGE:47699"
/clone="Organ: liver: Vector: pDNR-LIB (Clontech): Site_1: Sfil (ggccattatggcc): 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCGCATATGGCC 3' and 3' adaptor sequence: 5'-CACGGCCATATGGCC 3' and 3' adaptor sequence: 5'-CACGGCCATATGGCC 3' and 3' adaptor sequence: 5'-CACGGCCATATATGGCC 3' and 3' adaptor sequence: 5'-CACGGCCCACATG-GT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb): 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria: Primatesa Catarrhini; Hominidae: Homo.

Musta, Catarrhini; Hominidae: Homo.

Musta, Catarrhini; Hominidae: Homo.

Musta, Catarrhini; Homon, Catarrhini; Hominidae: Homo.

Musta, Catarrhini; Homon, Catarrhini; Homon, Catarrhini; Ca
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AV695838 GKC Homo sapiens cDNA clone GKCBEE06 5', mRNA sequence.
AV695838.1 GI:10297701
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.n.h.gov
Tissue procurement CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M. A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyt Genomics, Inc.
CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 11
High quality sequence stop: 718.
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/db_arref="taxon:9606"
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                                             Shanghai
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Homo sapiens cDNA GK- clones
Unpublished (2000)
Contact: Zeguang Huan
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Sha
701203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: harag@hgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                               Score 267.4; DB 10: Length 530;
Pred. No. 8e-63;
0; Mismatches 121; Indels 12;
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Best Local Similarity 74.7%;
Matches 392; Conservative (
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/dev_stage="Adult"
/lab_host="SOLR"
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/db_xref="taxon:9606"
/clone="GLCGJG12"
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Sequence

Sequence 2, Appli Sequence 1, Appli Sequence 10, Appli Sequence 20, Appl Sequence 22, Appli Sequence 23, Appli Sequence 24, Appli Sequence 24, Appli Sequence 1, Appli Sequence 14, Appli Sequence 14, Appli Sequence 15, Appli Sequence 15, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli

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GENERAL INFORMATION:
APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUENGER ELIZABET M. J.
APPLICANT: GILLAM, ELIZABET M. J.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
TITLE OF INVENTION: CYTOCHROME P450
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,981E
FILING DATE: February 10, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 163; DB 2;
Pred. No. 1.4e-42;
US-08-750-703-3

US-08-750-703-4

US-08-750-703-1

US-08-750-703-1

US-08-116-459-11

US-08-116-58D-20

5508199-3

US-08-145-658D-22

US-08-145-658D-22

US-08-145-658D-22

US-08-145-658D-21

US-08-145-658D-21

US-08-145-658D-21

US-08-145-658D-21

US-08-145-658D-24

US-08-133-448-45

US-08-133-448-45

US-08-133-448-45

US-08-233-463-14
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                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Elizabeth Selby
REGISTPATION NUMBER: 38,298
REFERCE/DOCKET NUMBER: 22000.0022
TELECOMMUNICATION INFORMATION:
TELEFAN: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 4:
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Patent No. 5886157
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97.18;
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LENGTH: 1419 base pairs
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US-08-194-981E-4
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     CITY:
       April 19, 2002, 08:10:30 ; Search time 130.44 Seconds (without alignments) 1290.043 Million cell updates/sec
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-194-981E-3
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US-08-238-8218-10
US-08-201-118-4
US-08-201-118-4
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PCT-US95-05744-4
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US-08-201-118-12
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PCT-US95-05744-8
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Length 1419;

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us-09-763-292-2.rni

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Sequence 10, Application US/08201118
Patent No. 5786191
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: RONKES-SPARKS, Marjorie
TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
TITLE OF INVENTION: SUBFAMILY
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
   224 IGGIGCIGCAIGGAIAIGAAGCAGIGAAGGAAGCCCIGAITGAICTIGGAGAGGAGIIII 283
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Pred. No. 1.6e-42;
O; Mismatches 5;
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ER: 15280-192-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION 1913
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/COCKET NUMBER: 15280-192-1
IELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,118 FILING DATE: 22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.98;
97.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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LENGTH: 1852 base pairs
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Best Local Similarity
Matches 166; Conserv
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US-08-238-821B-10
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                                                                                                                                       US-08-201-118-10
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                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                            ....<u>y</u>
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                                                                                              126 cctagctctcaaaggtctatggcctgtgttcactctgtattttggcctgaaacccatag 185
                                                               110 CCAATCTCTCAAAGGTCTATGGCCCTGTGTTCACTCTGTATTTTGGCCTGAAACCCATAG 169
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                                                                                                                                                                  Length 1591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 163; DB 2; Lengtu Lo. Pred. No. 1.5e-42;
 Indels
                                                                                                                                                                                                                                                                                                                                     APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUENGERICH, F. Peter
APPLICANT: SANDHU, Pumblu,
APPLICANT: SANDHU, Pumblu,
APPLICANT: SANDHU, Pumblu,
APPLICANT: SANDHU, Pumblu,
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
TITLE OF INVENTION: CYTOCHROME P450
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE 6 ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street, NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,981E
FILING DATE: February 10, 1994
 Š;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                      Sequency 3, Application US/08194981E Patent No. 5886157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Selby
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-9880
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.9%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 1591 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 97.1'
Matches 166; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Georgia
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TOPOLOGY: lir
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US-08-194-981E-3
Matches 166;
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PCT-US95-05744-10
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Sequence 10, Application US/08238821B
Patent No. 5912120
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: DE MORES-SPARKS, Marjorie
APPLICANT: DE MORIS, Sonia M.F.
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF STITLE OF INVENTION: WEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ċ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 ctggaagaggcattttcccactggctgaaagagctaacagaggatttggta 296
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/238,821B
FILING DATE: 06 MAY-1994
                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                              STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15280-192110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
AF-LICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
PROR APPLICATION DATA:
APPLICATION WUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15,
TELECOMMUNICATION:
TELEPHONE: (650) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEGENT 1852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 166; Conserv
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RESULT

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Sequence 10. Application PC/TUS9505744
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, JOYCE A.
APPLICANT: ROMES-SPARKS, Marjorie
APPLICANT: B. MORAIS, Sonia M.F.
TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
TITLE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSES ADDRESSES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 21.9%; Score 163; DB 5; Length 18 Best Local Similarity 97.1%; Pred. No. 1.6e-42; Matches 166; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                           Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA: PPLICATION NUMBER: PCI/US95/05744 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dow, Karen B. SEGISTATION WUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-192-1-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION WUMBER:
FILING DATE: 06-MAY-1994
PRIOR APPLICATION WUMBER: US 08/201,118
APPLICATION WUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
PRIOR APPLICATION WUMBER: US 07/864,962
APPLICATION WUMBER: US 07/864,962
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08201118
Patent No. 5786191
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2420
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and To
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: CDNA PCI-US95-05744-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                               94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-201-118-4
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ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650) 326-2422
INFORMATION FOR SED ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..12
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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es 156; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                         CITY: Sar
STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-238-821B-4
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Best Local Sin
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   GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, JOyce A.
APPLICANT: GOLDSTEIN, Marjorie
TILLE OF INVENTION: CLOMING AND EXPRESSION OF COMPLEMENTARY
TILLE OF INVENTION: SUBFAMILY
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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APPLICANT: ROWES-SPARKS, Marjorie
APPLICANT: ROWES-SPARKS, Marjorie
APPLICANT: DE WORALS, Sonia M.F.
TILLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TILLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL SETERMINANT OF STILLE OF INVENTION: MEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 461
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 cctagctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.9%; Score 163; DB 1; Length 1854; 97.1%; Pred. No. 1.6e-42; 1ve 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15280-192-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-ARR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICE.

FILING DATE: ...

ATORNEY/AGENT INFORMATICE.

NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15280-
TELEPHONE: (415) 326-2400
TELEFA: (415) 326-2402
TELEFA: (415) 326-3402
TELEFA: (415) 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08238821B
: Patent No. 5912120
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 97.1
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM IYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: CDNA
US-08-201-118-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-238-821B-4
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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176 CCAATCTCTCAAAGGTCTATGGCCCTGTGTTCACTCTGTATTTTGGCCTGAAACCCATAG 235
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Sequence 4, Application PC/TUS9505744

GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROMEES-SPARKS, Mariorie
APPLICANT: DE MORAIS, SONIA M.F.
IIILE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
IIILE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
IIILE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Corresponds to positions -12 to-1 for 25 of Figure 2."
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                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,821B
FILING DATE: U6-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
ATORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/POCKET NUMBER: 15280-192110US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-BOS/MS-DOS
OPERATING SYSTEM: PC-BOS/MS-DOS
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROWKES-SPARKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.
IIILE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
IIILE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
IIILE OF INVENTION: MEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 cctagctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 IGGIGNIGCAIGGATATGAAGCAGTGAAGCACCCTGATTGAICNTGGAGAGGAGTTTT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.6%; Score 153.4; DB 1; 91.8%; Pred. No. 2e-39;
                                                                                                                                           Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     15280-192-1
                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
BEFEDENSFY/DOCKET NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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: Patent No. 5912120
                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     TELEPRONE: (415) 326-2402
TELEPRA: (415) 326-2422
INFEMATION FOR SEO 1D NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1892 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 157; Conservative
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  California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE IYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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                                        94301
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                     COUNTRY:
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APPLICANT: GOLDSTEIN, Joyce A.

APPLICANT: GOLDSTEIN, Joyce A.

APPLICANT: GOLDSTEIN, Joyce A.

ITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY

ITLE OF INVENTION: DNAS FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C

TITLE OF INVENTION: SUBFAMILY

NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.9%; Score 163; DB 5; I ilarity 97.1%; Pred. No. 1.6e-42; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dow, Raren B.
REGISTRATION WUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-192-1-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/238,821
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
PRIOR APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/05744
                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08201118 Patent No. 5786191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
                 379 Lytton Avenue
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
    MOLECULE TYPE: CDNA
                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                FILING DATE
ALTARESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                    SOFTWARE:
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Best Local Simi
Matches 166;
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linear
                                                                 FILING DATE:
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                SOFTWARE:
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GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROMES-SPARKS, Marjorie
APPLICANT: ROMES-SPARKS, Sonia M.F.
TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
TITLE OF INVENTION: OF S-MEPHYNYIOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Corresponds to positions -41 to-1 for 2c of Figure 2."
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.6%; Score 153.4; DB 2; 91.8%; Pred. No. 2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                          15280-192110US
                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APPL199
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTATION NUMBER: 37,525
REFERENCE/DOCKET NUMBER: 15280-192111
TELECOMMUNICATION INFORMATION:
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,821B
FILING DATE: 06-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy'disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 326-2400
TELEFAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1892 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 91.83
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COTHER INFORMATION:
COTHER INFORMATION:
CS-08-255-821B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94301
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PCT-US95-05744-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 8
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GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, JOyce A.
APPLICANT: GOLDSTEIN, JOyce A.
APPLICANT: GOLDSTEIN, JOyce A.
APPLICANT: GOLDSTEIN, JOyce A.
IIILE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
TITLE OF INVENTION: SUBFAMILY
NUMBER OF INVENTION: SUBFAMILY
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 tggtgctgcatggatatgaagcaqtgaaggaagccctgattgatcttggaggagagtttt 245
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COMPUTER: IBM PC compatible
OPERATING SYSEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 153.4; DB 5;
Pred. No. 2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-192-1-1
TELECOMMUNICATION INFORMATION:
                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,821
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOW, KAIPEN B.
REGISTATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08201118
Patent No. 5786191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ 1D NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIREET: 379 Lytton Avenue CIIY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 1892 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 20.5
Best Local Similarity 91.8
Matches 157; Conservative
                  CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94301
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                                                                                                                                                                                                                                                                                                                                                                                                            US-08-238-821B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
PCT-US95-05744-2
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APPLICANT: BOMKES-SPARKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.
TITLE OF INVENTION: CLOCHROME PA50 2C19: THE PRINCIPAL DETERMINANT OF S-
TITLE OF INVENTION: WEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,821B
FILING DATE: U6-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         20.1%; Score 149.6; DB 1
97.4%; Pred. No. 3.2e-38;
tive 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      581 cgctgccttgtggaggagttgagaaaaccaagggt 616
                                                                                                                                            NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15280-192-1
TELECHUNICATION INFORMATION:
TELEFANT: (415) 326-2402
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACIERISTICS:
LENGTH: 1746 base pairs
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08238821B
Patent No. 5912120
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GOLDSTEIN, Joyce A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 97.48
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-238-821B-2
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Sequence 2, Application PC/TUS9505744

GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROWKES-SPARKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.
ITILE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
ITILE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
ITILE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 20.1%; Score 149.6; DB 2; Length 1746; Best Local Similarity 97.4%; Pred. No. 3.2e-38; Matches 152; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE CALIFORNIA CONTRACTOR CONTRAC
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581 cgctgccttgtggaggagttgagaaaaaccaagggt 616
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REGISTRATION NUMBER: 37,505
REFERENCE/COCKET NUMBER: 15280-192110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 326-2400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1746 base pairs
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATIORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,821
FILING DATE: 06-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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LOCATION: 1..5
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Sequence 13 Application US/08716459

Fatent No. 5821062.

GENERAL INFORMATION:

APPLICANT: KANEKO, Hideo

APPLICANT: KANEKO, Hideo

TILLE OF INVENTION: OLICONUCLEOTIDE FOR USE IN CHECKING

TILLE OF INVENTION: HUMAN-DERIVED CYTOCHROME P45011C13 GENE

NUMBER OF SEQUENCES:

ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP

STREET P.O. Box 747

CITY: Falls Church

STAME: Virginia

STAME: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.1%; Score 149.6; DB 5 97.4%; Pred. No. 3.2e-38; Live 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            581 cgctgccttgtggaggagttgagaaaaaccaagggt 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 CGCTGCCTTGTGGAGGAGTTGAAAAAACCAAGGCT 488
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC

COMPUTER: IBM PC

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

FILLING DATE: 27 SEPTEMBER 1996

CLASSIFICATION: 536
                                                                                                                     NAME: DOW, KAICH B.
REGISTRATION NUBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-192-1-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2402
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION DATA:
APPLICATION NUMBER: JP-059385/1994
APPLICATION NUMBER: JP-059386/1994
FILING DATE: 29-03-1994
FILING DATE: 29-03-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-ARR-1992
ATTUREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         LENGTH: 1746 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLXX: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 152; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-05744-2
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Gaps
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                                                                                                                                                                                    DNA fragment obtained by
                                                                                                                                                                                                                                                       Score 144; DB 1; Length 200;
Pred. No. 5.8e-37;
0; Mismatches 20; Indels
                     REFERENCE/DOCKET NUMBER: 20-4081PCT TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: April 19, 2002, 08:10:39 Job time: 2939 sec
                                                                                                                                                                      : TOPOLOGY: linear

: MOLECULE TYPE: Other nucleic acid

: MOLECULE TYPE: cloning

US-08-716-459-13
ard R.
30,330
                                                  TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8050 TELEX: 248345 INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.6%;
Matches 156; Conservative
SVENSSON, Leonard
                                                                                                                          LENGTH: 200
TYPE: nucleic acid
STRANDEDNESS: single
            REGISTRATION NUMBER:
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